Publication number:

0 675 200 A1

(2)

EUROPEAN PATENT APPLICATION

21 Application number: 94117761.0

2 Date of filing: 10.11.94

(1) Int. Cl.⁶: C12N 15/19, C07K 14/52, C12N 15/62, C12N 1/21, C12N 1/19, C12N 5/10, C07K 16/24, C12N 15/11, G01N 33/68

Priority: 10.11.93 JP 305975/93 13.12.93 JP 342526/93 18.03.94 JP 74344/94 08.07.94 JP 180955/94 07.09.94 JP 239363/94 18.10.94 JP 278378/94

Date of publication of application: 04.10.95 Bulletin 95/40

Designated Contracting States: AT BE CH DE DK ES FR GB GR IE IT LI LU MC **NL PT SE**

Applicant: MOCHIDA PHARMACEUTICAL CO., LTD. 7, Yotsuya 1-chome Shinjuku-ku Tokyo 160 (JP) Applicant: OSAKA BIOSCIENCE INSTITUTE 2-4, Furaedai 6-chome Suita-shi, Osaka 565 (JP)

Inventor: Nagata, Shigekazu 21-17-511, Saidera 2-chome Sulta-shi, Osaka-fu (JP) Inventor: Suda, Takashi

4-20-302, Onohara Higashi 3-chome

Minou-shi. Osaka-fu (JP)

Inventor: Takahashi, Tomohiro, c/o MOCHIDA

PHARMACEUTICAL

CO., LTD.

7, Yotsuya 1-chome

Shinjuku-ku,

Tokyo (JP)

Inventor: Nakamura, Norio, c/o MOCHIDA

PHARMACEUTICAL

CO., LTD,

7, Yotsuya 1-chome

Shinjuku-ku,

Tokyo (JP)

(4) Representative: Grünecker, Kinkeldev, Stockmair & Schwanhäusser Anwaltssozietät

Maximilianstrasse 58

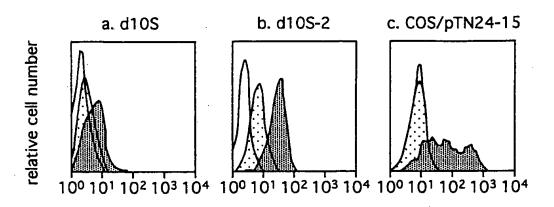
D-80538 München (DE)

A FAS ligand, a fragment thereof and DNA encoding the same.

This invention provides a novel polypeptide useful in the field of medicines, a novel DNA which encodes the novel polypeptide, a recombinant DNA molecule which contains the novel DNA, a transformant transformed with the novel DNA or the recombinant DNA molecule, a process for the purification of the novel polypeptide, a process for the production of the novel polypeptide, an antibody which recognize the novel polypeptide, an oligonucleotide complementary to the novel DNA and a novel screening method.

Particularly this invention provides a novel polypeptide which is Fas ligand or a fragment thereof. This novel polypeptide can be used as an effective ingredient of a medicament for regulating the apoptosis in a living body. This novel polypeptide is obtained by identifying a DNA fragment which encodes the novel polpeptide, transforming a desired host with a recombinant DNA molecule which contains the DNA fragment and purifying the novel polypeptide produced by the resulting transformant. This novel polypeptide has a cytoplasmic domain, a transmembrane domain and extracellular domain and takes part in apoptosis.

FIG.1



fluorescence intensity

FIELD OF THE INVENTION

This invention relates to a Fas ligand, a part of the Fas ligand and a novel DNA fragment which encodes the Fas ligand, which may be utilized in the field of medicines. This invention also relates to an antibody which can be used for detecting of the Fas ligand, which may be utilized in the field of diagnostic reagents. This invention also relates to a recombinant DNA molecule which contains the novel DNA fragment, a transformant, a process for purifying the novel protein and a process for producing of the novel protein. This invention also relates to an antisense oligonucleotide.

BACKGROUND OF THE INVENTION

Based on the morphology of dying cells, Cell death is generally divided into two categories, necrosis and apoptosis. In the necrotic cell death, degradation of cell membrane and release of cellular contents into extracellular matrix are observed. On the other hand, in the apoptotic cell death, fragmentation of chromosomal DNA and concentration of nuclei are observed while the degradation of the cell membrane and the release of the cellular contents as observed in the necrosis are not observed. Apoptosis has been conceived to be a form of programmed cell death. For example, phenomena of deletion of unnecessary cells and organs in the course of ontogenesis are considered to be caused by the apoptosis of cells. Another phenomenon that is considered to be the apoptosis is the cell death which occurs when virus-infected cells and tumor cells are attacked and removed by cytotoxic T cells (CTL), natural killer cells (NK cells), $TNF_{-\alpha}$, $TNF_{-\beta}$ and the like. As described above, apoptosis is one of the physiological phenomena which have recently attracted special attention, and studies are being conducted by many researchers with the aim of elucidating the function of the apoptosis as well as its physiological meaning and relation to diseases.

Fas antibody has been known as a substance which can induce the apoptosis of cells. Fas antibody is a monoclonal antibody obtained by immunizing a mouse with human fibloblast (Yonehara S. et al., J. Exp. Med., vol. 169, pp. 1747 - 1756, 1989). Since Fas antibody has been obtained by the immunization of a mouse with cells, the type of molecules recognized by Fas antibody and the transfer mechanism of apoptosis signal to the cells were not revealed for a long time. Recently, however, Itoh N. et al. have succeeded in cloning the gene of the molecule (Fas antigen) which is specifically recognized by the Fas antibody (Cell, vol. 66, pp. 233 - 243, 1991). It was then found that the Fas antigen is a cell membrane protein having a size of about 45 kD, and its amino acid sequence analysis has revealed that the Fas antigen belongs to the family of TNF receptors. In addition, a mouse Fas antigen gene was cloned (Watanabe-Fukunaga R. et al., J. Immunol., vol. 148, pp. 1274 - 1279, 1992), and the mRNA for Fas antigen was confirmed to be expressed in thymus, liver, lung, heart and ovary of the mouse.

After the cloning of the Fas antigen gene, a number of studies have been conducted and reported on the relationship between the apoptosis mediated by Fas antigen and various diseases.

Kobayashi N. et al. have reported that expression of Fas antigen on T cell membrane is induced upon infection with AIDS virus, suggesting a possibility that the apoptosis of T cells found in AIDS is a Fas antigen-mediated phenomenon (Nikkei Science, vol. 6, pp. 34 - 41, 1993).

Ogasawara J. et al. have observed that a phenomenon similar to fulminant hepatitis occurs upon administration of Fas antibody to a mouse, and suggested a possibility of the occurrence of a Fas antigenmediated apoptosis in the inflammatory lesion of the fulminant hepatitis or the like (*Nature*, vol. 364, pp. 806 - 809, 1993). Hiramatsu Y. et al. have reported that, in a patient suffering chronic type C hepatitis, Fas antigen is frequently expressed in the inflammatory lesion of the liver where leukocyte infiltration is observed (Hepatology, vol. 19, pp. 1354 - 1359, 1994).

In addition, Watanabe-Fukunaga R. et al. have confirmed that a mutation in the Fas antigen gene is present in the lpr mouse, which is one of autoimmune disease model animals and that the cells expressing such mutation in the Fas antigen gene do not undergo the apoptosis (Nature, vol. 356, pp. 314 - 317, 1993). Watanabe-Fukunaga R. et al. have estimated that autoimmune disease-like symptoms are generated by the autoreactive T cells remaining in the body, that should have been removed from the body through the apoptosis.

As described above, a number of studies have been reported on the relation between the Fas antigen and diseases. An unsolved question is whether or not there is a molecule (Fas ligand) that binds to the Fas antigen on the cell surface to induce the cell apoptosis, namely, a molecule that acts in a manner similar to the above described Fas antibody.

Watanabe-Fukunaga R. et al. have presumed that, in a gld mouse which exhibits autoimmune diseaselike symptoms, an abnormality should be present in a biological molecule which binds to Fas antigen, as in the case of the lpr mouse.

In addition, Rouvier E. et al. have reported that a certain type of T cells show a specific cytotoxic action on the cells expressing Fas antigen (*J. Exp. Med.*, vol. 177, pp. 195 - 200, 1993). More illustrating, they have shown that a Ca²⁺-independent cytotoxic action by mouse peripheral blood lymphocytes (PBL) and PC60-d10S cells, the latter being a hybridoma of mouse CTL and rat T-lymphoma cells, is observed only for the Fas antigen-expressing cells. They have also suggested the possibility that such lymphocytes, especially T cells, could recognize the Fas antigen or certain Fas antigen-related molecules, and the possibility that these cells might express to Fas ligand.

Though the possibility of the presence of a Fas ligand has been suggested by the researchers as described above, its specific nature is not yet revealed.

It is important to isolate the Fas ligand in order to elucidate mechanism of the Fas antigen-mediated apoptosis and reveal relationship between the Fas antigen-mediated apoptosis and diseases more clearly. In consequence, confirmation of the presence of the Fas ligand and revelation of its true nature have been called for in various fields including the medicine.

A primary object of the present invention is to provide the field of medical care with a Fas ligand and its gene and a means for artificially regulating apoptosis generated in the body.

As described in the foregoing, the diseases considered to be related to the Fas antigen-mediated apoptosis include those which are caused by the Fas antigen-mediated apoptosis, and, those which are caused by the absence of the Fas antigen-mediated apoptosis. For example, it is estimated that death of hepatocytes and the subsequent reduction in the liver function in the case of hepatitis and decrease in the number of HIV-infected T cells and the subsequent reduction in the immunological function in the case of AIDS would be improved by inhibiting the apoptosis. In the case of certain autoimmune diseases, on the other hand, the symptoms are estimated to be improved by allowing the Fas antigen-mediated apoptosis to occur normally and by enhancing the removal of autoantigen reactive T cells. With regard to the treatment of AIDS in its early stage, induction of the apoptosis of the cells infected with HIV and their removal from the body would be effective. Morimoto H. et al. have reported that the Fas antigen-mediated apoptosis induced in cancer cells could synergistically enhance carcinostatic effects of adriamycin and cisplatin (Cancer Res., vol. 53, pp. 2591 - 2596, 1993). A substance capable of binding to Fas antigen to induce apoptosis should be useful in the treatment of cancers.

Such a treatment which is based on the principle of artificially regulating the Fas antigen-mediated apoptosis can be established only after the identification of the Fas ligand. In other words, artificial enhancement of the apoptosis in the living body would be enabled when the Fas ligand is specified.

In order to use the Fas ligand or a part of the ligand in medical treatments and researches, it would be necessary to produce the Fas ligand protein in a large scale and at a high purity. Cloning of the gene coding for such protein will enable the production of the protein by means of genetic engineering techniques, and the thus produced protein can be used for the main effective component in therapeutic drugs and in the production of antibodies. In addition, the gene itself could be used in gene therapy and development of antisense drugs, as well as for the preparation of model animals, such as transgenic mice, of apoptosis-related diseases.

SUMMARY OF THE INVENTION

40

55

The inventors of the present invention have conducted intensive studies with the aim of isolating Fas ligand, taking note of the aforementioned PC60-d10S cells. PC60-d10S is a hybridoma of mouse CTL and rat T-lymphoma, which induces apoptosis only in Fas antigen-expressing cells when stimulated with PMA (phorbol myristate acetate) and ionomycin. As a result of intensive studies, the present inventors have succeeded in obtaining a cell population, PC60-d10S-2, which shows higher cytotoxicity without stimulation and is useful for the cloning of the Fas ligand gene. Thereafter, the rat Fas ligand gene was cloned making use of this cell population. Also, the present inventors have conducted intensive studies with the aim of isolating a human Fas ligand suitable for use in pharmaceutical drugs and the like and succeeded in obtaining a gene which encodes human Fas ligand, as well as a gene which encodes mouse Fas ligand. It was confirmed thereafter that these genes have similar sequences having a common partial sequence. The inventors of the present invention have also identified the part of the sequence that should be necessary in exhibiting Fas ligand function. The present invention has been accomplished on the basis of these efforts.

According to first aspect of the present invention, there is provided a polypeptide which is a Fas ligand. According to second aspect of the present invention, there is provided a fragment of the Fas ligand polypeptide according to the first aspect of the invention.

According to third aspect of the present invention, there is provided a DNA fragment containing a nucleotide sequence coding for the polypeptide according to the first or second aspect of the invention.

According to fourth aspect of the present invention, there is provided a recombinant DNA molecule including the DNA according to the third aspect of the invention.

According to fifth aspect of the present invention, there is provided a transformant which has been transformed with the DNA fragment according to the third aspect of the invention.

According to sixth aspect of the present invention, there is provided a transformant which has been transformed with the recombinant DNA molecule according to the fourth aspect of the invention.

According to seventh aspect of the present invention, there is provided a process for producing the polypeptide according to the first or second aspect of the invention wherein the transformant according to the fifth or sixth aspect of the invention is used.

According to eighth aspect of the present invention, there is provided a process for purifying the polypeptide of the first or second aspect of the invention.

According to ninth aspect of the present invention, there is provided an antibody capable of recognizing the polypeptide according to the first or second aspect of the invention.

According to tenth aspect of the present invention, there is provided an oligonucleotide or a derivative thereof which includes a nucleotide sequence which is complementary to a part of a Fas ligand gene or a part of mRNA for the Fas ligand.

According to eleventh aspect of the present invention, there is provided a process for screening a Fas ligand-related substance wherein the polypeptide according to the first or second aspect of the invention, or a transformant capable of expressing the polypeptide according to the first or second aspect of the invention is used.

Other objects and advantages of the present invention will become apparent as the description progresses.

BRIEF DESCRIPTION OF THE DRAWINGS

25

35

40

50

55

- Fig. 1; a, b and c show the results of flow cytometry of COS-7 cells transformed with d10S, d10S-2 or pTN24-15, respectively.
- Fig. 2 shows the nucleotide sequence in clone pTN24-15 and the amino acid sequence deduced therefrom.
 - Fig. 3 shows the nucleotide sequence in clone pTN24-15 and the amino acid sequence deduced therefrom.
 - Fig. 4 shows the results of northern hybridization of d10S, d10S-2 and d10S-16.
 - Fig. 5 shows the results of northern hybridization of rat splenocytes and thymocytes.
 - Fig. 6 shows the results of northern hybridization of rat tissues.
 - Fig. 7 shows the results of immunoprecipitation of COS-7 cells transformed with d10S-12 or pTN24-15.
 - Fig. 8 shows cytotoxic activity of d10S cells when W4 and W19L are used as target cells.
 - Fig. 9 shows cytotoxic activities of COS-7 cells transformed with pTN24-15 and COS-7 cells transformed with pCEV4 when W4 and W19L are used as target cells.
 - Fig. 10 shows cytotoxic activities of COS-7 cells transformed with pTN24-15 and COS-7 cells transformed with pCEV4 when W4 and W19L are used as target cells.
 - Fig. 11 shows the inhibition effect of mFas-Fc on cytotoxic activity of COS-7 cells transformed with d10S cells or pTN24-15 against W4 cells.
- Fig. 12 shows gel electrophoresis showing changes in the chromosomal DNA in target cells when COS-7 cells transformed with pTN24-15 are used as effector cells and W4 and W19L cells are used as the target cells.
 - Fig. 13 shows the results of SDS-polyacrylamide electrophoresis of purified Fas ligand.
 - Fig. 14 shows cytotoxic activity of purified Fas ligand when W4 and W19L cells are used as target cells.
 - Fig. 15 shows the nucleotide sequence of plasmid pBL-hFL4H and the amino acid sequence deduced therefrom.
 - Fig. 16 shows the nucleotide sequence of human Fas ligand chromosomal gene.
 - Fig. 17 shows the nucleotide sequence of human Fas ligand chromosomal gene.
 - Fig. 18 shows the nucleotide sequence of human Fas ligand chromosomal gene.
 - Fig. 19 shows the nucleotide sequence in clone pBX-hFL1.
 - Fig. 20 shows the nucleotide sequence in clone pBX-hFL1.
 - Fig. 21 shows cytotoxic activity of COS cells transformed with pEX-hFL1 and COS cells transformed with pEF-MFLW4F when WR19L and WC8A are used as target cells.

Fig. 22 shows inhibition effect of hFas-Fc and mFas-Fc on cytotoxicity of COS cells transformed with pBL-hFL1 against WC8A cells.

Fig. 23 shows the nucleotide sequence in clone pBL-MFLW4 and the amino acid sequence deduced therefrom.

Fig. 24 shows the nucleotide sequence in clone pBL-MFLW4 and the amino acid sequence deduced therefrom.

Fig. 25 shows cytotoxic activity of COS cells transformed with pEF-MFLW4F when WR19L and W4 are used as target cells.

Fig. 26 shows cytotoxic activity of COS cells transformed with a plasmid containing Fas ligand cDNA isolated from gld mice when WR19L and W4 are used as target cells.

Fig. 27 is a photograph showing the results of the western blotting in which antiserum 19-3 and human Fas ligand-expressing cells are used.

Fig. 28 is a photograph showing the results of the western blotting in which a monoclonal antibody F864-5-1 and human Fas ligand-expressing cells are used.

Fig. 29 shows reactivity of monoclonal antibody F883-1-1 with a peptide.

Fig. 30 shows apoptosis inhibiting activity of monoclonal antibody F883-1-1.

Fig. 31 shows reactivity of monoclonal antibody F897-1-2 with peptide (3).

Fig. 32 shows apoptosis inhibiting activity of monoclonal antibody F897-1-2.

Fig. 33 shows cytotoxic activity of the culture supernatant of transformant COS-1/pM1070 when WC8 and W4 are used as target cells.

Fig. 34 shows cytotoxic activity of a culture supernatant of transformant COS-1/pEX-hFL1 when WC8 and W4 are used as target cells.

Fig. 35 is a photograph showing the results of the western blotting of a culture supernatant of the transformant COS-1/pM1070 carried out under non-reducing condition.

Fig. 36 is a photograph showing the results of the western blotting of a culture supernatant of the transformant COS-1/pEX-hFL1 carried out under non-reducing condition.

Fig. 37 shows apoptosis inhibiting activity of antisense oligomer A41.

Fig. 38 shows apoptosis inhibiting activity of antisense oligonucleotides A69, A184, A355, A505, A733 and A924.

Fig. 39 shows cytotoxic activity of polypeptides ND38, ND40, ND41, ND42, ND43 and CD179 respectively in culture supernatant.

Fig. 40 is a photograph showing the results of the western blotting in which transformant JE5505 (pM1068) and culture supernatant thereof are used.

Fig. 41 is a photograph showing the results of the western blotting in which transformant JE5505 (pM1069) and culture supernatant thereof are used.

DETAILED DESCRIPTION OF THE INVENTION

25

30

The present invention is hereinafter described in further detail.

First, the polypeptide according the first aspect of the present invention is described.

In the description of the present invention, the term, "polypeptide containing (or including) the amino acid sequence of formula X (or SEQ ID NO: X)" designates the polypeptide having the amino acid sequence defined in formula X (or SEQ ID NO: X) wherein one or more amino acid residues are optionally added on either one or both of its N terminus and C terminus.

The term, "polypeptide having the amino acid sequence of formula X (or SEQ ID NO: X)" designates the polypeptide having the amino acid sequence defined in formula X (or SEQ ID NO: X).

The term, "Fas ligand" designates a substance provided with an activity to induce apoptosis of a Fas antigen-expressing cell. Apoptosis of the Fas antigen-expressing cells is estimated to have been induced by the binding of the Fas ligand with the Fas antigen on the cell surface, which results in the transfer of the apoptosis signal to the cell via the Fas antigen.

The "Fas antigen" as used herein may be any Fas antigen of animal origin including human Fas antigen, rat Fas antigen and mouse Fas antigen. In this connection, amino acid sequence of human Fas antigen has been determined by Itoh, N. et al., Cell, vol. 66, pp. 233-243, 1991. Amino acid sequence of mouse Fas antigen has been determined by Watanabe-Fukunaga, R. et al., J. Immunol., vol. 148, pp. 1274-1279, 1992. Amino acid sequence of rat Fas antigen has been determined by Kimura, K. et al., Biochem. Biophys, Res., Commun., vol. 198, pp. 666-674, 1994.

The polypeptides according to the first aspect of the present invention may include any one of the sequences defined in formulae 1 to 12.

The amino acid sequences defined in formulae 1 to 4 are the amino acid sequences of the Fas ligands of human cell origin. The amino acid sequences defined in formulae 5 to 8 are the amino acid sequences of the Fas ligands of rat cell origin. The amino acid sequences defined in formulae 9 to 12 are the amino acid sequences of the Fas ligands of mouse cell origin.

The amino acid sequences defined in formulae 4, 8, and 12 includes all the intracellular, transmembrane, and extracellular domains, and it is estimated that such polypeptides should exist in organisms as cell surface polypeptides. Therefore, production of polypeptides with such amino acid sequences would require purification of the polypeptides from the cells or tissue expressing such polypeptides.

The extracellular domain of a cell surface polypeptide is often cleaved off the cell membrane to be released into the supernatant of the cell culture producing such polypeptide or into body fluids such as urine and blood. In general, purification of a polypeptide is more efficient and productive when the polypeptide is purified from a supernatant or urine compared to the purification from cells or a tissue. The situation is the same for the Fas ligand, and purification of the extracellular domain of the Fas ligand is more productive than the purification of the entire Fas ligand.

In the present invention, there is also provided polypeptides corresponding to such extracellular domain of the Fas ligands. The cleavage site of the Fas ligand at which the extracellular domain is separated from the cell membrane is not limited to any particular site, and the cleavage site may vary according to the conditions of the cell culture or proteases present inside or outside the cell. Preferably, the extracellular domains of the Fas ligands are polypeptides having the amino acid sequences defined in formulae 3, 7 and 11, which correspond to the extracellular domains of the human, rat, and mouse Fas ligands, respectively. The amino acid sequence of formula 3 corresponds to the sequence of from 103rd amino acid residue to 281st amino acid residue from the N terminus in the amino acid sequence of formula 4. The amino acid sequence of formula 7 corresponds to the sequence of formula 8. The amino acid sequence of formula 11 corresponds to the sequence of formula 8. The amino acid sequence of formula 11 corresponds to the sequence of formula 12.

As is known in the art, in producing polypeptides by recombinant DNA technology, amount of the polypeptide expressed, and hence, production efficiency would be higher when the polypeptide produced has a lower molecular weight. In addition, a polypeptide solely comprising the part required for its action would have an antigenicity lower than the polypeptides including additional sequences. Furthermore, if the polypeptide of interest has a low molecular weight, it would be possible to fuse the polypeptide with another polypeptide having another activity to provide the polypeptide with another activity, or to bind the polypeptide with an antibody to specify the target cell to which the polypeptide exerts its activity. In the present invention, there is provided polypeptides having the amino acid sequence defined by formula 1, 5 and 9 which have lower molecular weight, therefore, higher productivity and lower antigenicity are expected. There is also provided in the present invention polypeptides having the amino acid sequences defined by formula 2, 6 and 10.

Formulae 1, 2, 5, 6, 9 and 10 respectively represent parts of the amino acid sequences of the extracellular domain of the human, rat and mouse Fas ligands.

More illustratively, the amino acid sequences of formulae 1, 5 and 9 respectively represent the amino acid sequences of formulae 3, 7 and 11 wherein 42 amino acid residues on their N terminus are missing; and the amino acid sequences of formulae 2, 8 and 10 respectively represent the amino acid sequences of formulae 3, 7 and 11 wherein 41 amino acid residues on their N terminus are missing. As demonstrated in the Examples, the polypeptides (of formulae 1 and 2) having the amino acid sequences of formula 3 wherein 42 or 41 amino acid residues on the N terminus are missing still have the apoptosis-inducing activity. The polypeptides having the amino acid sequences of formula 3 wherein 40,38 or 34 amino acid residues on the N terminus are missing also have the apoptosis-inducing activity.

It was then indicated that the amino acid sequence in the downstream from the 43rd amino acid residue should be critical for the apoptosis-inducing activity, and a polypeptide including such critical sequence as defined by formula 1, 5 or 9 as a part of its sequence would have the apoptosis-inducing activity. Accordingly, the polypeptides of the present invention may be characterized by the inclusion of the amino acid sequence defined by formula 1, 5 or 9.

Of the polypeptides according to the first aspect of the present invention, the polypeptides having the amino acid sequence of formula 3 corresponding to the extracellular domain of the Fas ligand of human origin wherein amino acid residues of a number selected from 1 to 42 on the N terminus are missing are favorable in view of their lower antigenicity for human in comparision with Fas ligands of animal origin and higher productivity due to the lower molecular weight. Such polypeptides can also be collected from the culture supernatant when they are expressed with a suitable signal peptide by a transformant. In particular,

the polypeptides having the amino acid sequence of formula 3 wherein 40 or 34 amino acid residues on the N terminus are missing is favorable in view of its high activity.

In general, depending on the difference in species and individuals, mutation of amino acid sequence sometimes occurs in protein without spoiling its basic function. The term "mutation of amino acid sequence" as used herein means deletion of one or more amino acid residues from an amino acid sequence or their substitution by other amino acid residues and insertion or addition of one or more amino acid residues into or to optional sites of the amino acid sequence. Such a mutation can be introduced artificially by means of genetic engineering techniques.

In consequence, polypeptides having other amino acid sequences, for example, having derivatives of any one of the aforementioned amino acid sequences represented by the formulae 1 to 12 in which mutation of amino acid sequence occurred at one or more optional positions, are also included in the polypeptide of the present invention, provided that these polypeptide are possessed of similar properties of the polypeptide of the present invention.

In general, DNA molecules which encode polypeptide having the same function show mutual homology and hybridize each other in many cases. Diversity of amino acid sequences also occurs in many cases within such a range that DNA molecules encoding them can be hybridized each other. For example, as will be described later in EXAMPLES, DNA fragments which encode amino acid sequences of the aforementioned formulae 3 and 11 can hybridize with a DNA fragment which encodes amino acid sequences of the aforementioned formula 7. In addition, the Fas ligand which contains the amino acid sequence of the formula 3 can bind not only to human Fas antigen but also to mouse Fas antigen. Also, the Fas ligand which contains the amino acid sequence of the formula 7 can bind not only to rat Fas antigen but also to mouse Fas antigen. The Fas ligand which contains the amino acid sequence of the formula 11 can bind not only to mouse Fas antigen but also to human Fas antigen. Thus, it is considered that polypeptides having amino acid sequences encoded by mutually hybridizable DNA fragments have substantially the same function. In consequence, the novel polypeptide of the present invention characterized in that it contains an amino acid sequence encoded by a nucleotide sequence that hybridizes with a nucleotide sequence complementary to any one of the nucleotide sequences coding for the aforementioned amino acid sequences of formulae 1 to 12, preferably, formulae 1, 5, or 9.

In addition to the above mentioned features, the novel polypeptide of the present invention is preferably characterized in that it binds to at least one selected from the group consisting of human Fas antigens, rat Fas antigens and mouse Fas antigens, and more preferably, it shows an activity to induce apoptosis in Fas antigen-expressing cells.

Next, the polypeptide according to the second aspect of the present invention is described.

The polypeptide according to the second aspect of the present invention may comprise a fragment of a Fas ligand, or a fusion product of a plurality of the same or different fragments of the Fas ligand. Such polypeptide may preferably have a part of the amino acid sequence defined by any one of formulae 4, 8 and 12, and such polypeptide may be fused in an arbitrary order to constitute fusion polypeptides.

The polypeptide having a part of the amino acid sequence defined by formula 4, 8 or 12 may have any desired length. The polypeptide, however, may preferably have a length of 5 or more amino acid residues, and more preferably, a length of 10 or more amino acid residues to enable the inclusion the characteristic part of the amino acid sequence defined by formula 4, 8 or 12.

The polypeptide according to the second aspect of the present invention may be either capable or incapable of binding with the Fas antigen. Of the polypeptides according to the second aspect of the present invention, those capable of binding with the Fas antigen, but incapable of inducing the apoptosis, may be used as a substance that competitively acts against the Fas ligand in an organism, and such polypeptides may be administered for the purpose artificially inhibiting the apoptosis. As demonstrated in the Example, the polypeptide according to the second aspect of the present invention may be used as an antigen in producing an antibody against the polypeptide of the first aspect of the invention, irrespective of the presence or the absence of the binding ability with the Fas antigen or the apoptosis-inducing activity.

As described above, the polypeptide according to the second aspect of the present invention may comprise a fusion of two or more polypeptides each having the amino acid sequence which is a part of the amino acid sequence defined by formula 4, 8 or 12, which has been fused in an arbitrary order. Exemplary such fusion polypeptides include, a fusion of two polypeptides each having the amino acid sequence which is a part of the amino acid sequence defined by formula 4; and a fusion of a polypeptide having the amino acid sequence which is a part of the amino acid sequence defined by formula 4 with a polypeptide having the amino acid sequence which is a part of the amino acid sequence defined by formula 8 or 12. A preferred example are the polypeptide comprising the amino acid sequence of from 50th amino acid residue to 179th amino acid residue from the N terminus in the amino acid sequence defined by formula 3

fused to the C-terminus of the polypeptide comprising the amino acid sequence of from 1st amino acid residue to 49th amino acid residue from the N terminus in the amino acid sequence defined by formula 7 or 11. Such fusion polypeptides are chimera polypeptides of the Fas ligand of human origin with the Fas ligand of rat and mouse origin, respectively. Such fusion polypeptides are expected to have the apoptosis-inducing activity on Fas antigen-expressing cells.

The fusion polypeptide as described above may be produced with recombinant DNA technology by ligating the DNAs respectively coding for the polypeptide components to produce a DNA coding for the chimera Fas ligand; introducing the thus produced DNA in a suitable expression vector to transform a suitable host cell; and collecting the chimera Fas ligand of interest from the transformant cells or the culture supernatant.

The novel polypeptide according to the first and the second aspect of the present invention may have or may not have sugar chain.

Each of the amino acid sequences represented by the aforementioned formulae 4 and 8 contains 4 sites to which a sugar chain can be added (N-glycosylation sites). That is, amino acid residues of the positions 76 to 78, 184 to 186, 250 to 252 and 260 to 262 in the formula 4 and those of the positions 116 to 118, 130 to 132, 247 to 249 and 257 to 259 in the formula 8 correspond to the N-glycosylation sites. Also, the amino acid sequence of the aforementioned formula 12 has 5 N-glycosylation sites (amino acid residues of the positions 117 to 119, 131 to 133, 182 to 184, 248 to 250 and 258 to 260).

In consequence, addition of sugar chains to such polypeptides may occur when they are produced by animal cells or by means of genetic engineering techniques using eucaryotic cells such as of yeast and animals as the host. On the other hand, the novel polypeptide does not have a sugar chain when produced by means of genetic engineering techniques using procaryotic cells such as of *Escherichia coli* as the host.

Irrespective of the presence or the absence of additional sugar chains, the polypeptides according to the first and the second aspect of the present invention are useful, and may be used as the antigen in producing the antibody according to the ninth aspect of the present invention, or in screening the substances that would bind to such polypeptides.

The novel polypeptide of the first and the second aspects of the present invention may be produced by any method. For example, it may be chemically synthesized using a peptide synthesizer (e.g., Peptide Synthesizer 430A, Perkin-Elmer Japan) or purified from tissues, cells or body fluids of human and any other organism. Examples of the body fluids of human and animals include blood, urine and the like. Useful cells may be selected optionally from those which are capable of producing the novel polypeptide of the present invention. For example, cells capable of expressing the novel polypeptide of the present invention in a high quantity may be selected from splenocytes, thymocytes, lymphocytes and established cell lines thereof, through their analysis by northern blotting, western blotting and the like.

If necessary, production of the polypeptide may be induced by stimulating the cells with one or more appropriate stimulating agent selected from PMA (phorbol myristate acetate), ionomycin, PHA (phytohemagglutinin), ConA (concanavalin A), IL-2 (interleukin-2) and the like. Thereafter, the protein of interest is purified from the cells or a culture supernatant of the cells. Its purification may be carried out through an appropriate combination of usually used polypeptide purification steps such as concentration, various types of chromatography, salting out and the like, making use of the affinity of the polypeptide for Fas antigen or its cytotoxicity on Fas antigen-expressing cells as a marker. A preferred example of the purification method will be described later in relation to the eighth aspect of the present invention.

Preferably, however, the novel polypeptide may be produced by means of genetic engineering techniques in the form of a recombinant polypeptide in view of its purity. In order to obtain the novel polypeptide by means of genetic engineering techniques, appropriate host cells are transformed with the novel DNA of the third aspect of the present invention or the recombinant DNA molecule of the fourth aspect of the present invention, both of which will be described later, and the thus obtained transformant is cultured to recover the culture mixture with the transformant from which the polypeptide of interest is subsequently purified. The novel polypeptide may also be produced by another genetic engineering means making use of the novel DNA or the recombinant DNA molecule by employing a cell-free synthesis method (Sambrook J. et al., Molecular Cloning 2nd. ed., 1989).

A preferred example of the process for the production of the novel polypeptide of the present invention by means of genetic engineering techniques will be described later in relation to the seventh aspect of the present invention.

Recent advance in protein engineering techniques has made possible to bind polypeptide to high molecular compounds such as polyethylene glycol, styrene-maleic acid copolymer, dextran, pyran copolymer, polylysine and the like, as well as to natural high molecular compounds such as polysac-

charides, polypeptides and the like, physiologically active substances such as hormones and inorganic compounds such as magnetite and the like (see for example, *Proc. Natl. Acad. Sci. USA*, vol. 84, pp. 1487 - 1491, 1981, and *Biochemistry*, vol. 28, pp. 6619 - 6624, 1989).

An example of the binding method of polypeptide to polyethylene glycol is described briefly in the following. Firstly, a polypeptide of interest is dissolved in a buffer solution having a basic pH value within such a range that activity of the polypeptide is not spoiled. The thus prepared solution is mixed with an activated polyethylene glycol such as methoxypolyethylene glycol succinimidyl succinate to react with each other at room temperature for a certain period of time. Thereafter, a fraction having the activity of the polypeptide is collected by gel filtration or the like means.

The novel polypeptide of 1st and second aspect of the present invention can also be modified in such a manner through a combination of known techniques. In consequence, the novel polypeptide of the first and second aspects of the present invention also include those which received such modifications.

It is generally known that polypeptides often take the form of multimer by covalent bonding or non-covalent bonding in an organism or in a culture medium. Such multimer is formed by the binding of the polypeptides of the same type or different types. For example, TNF has been known to form a trimer, and actibin has been known to form a dimer.

The polypeptide according to the first and the second aspect of the present invention may be present either in the form of a monomer or a multimer. For example, the polypeptide of the present invention having the amino acid sequence defined by any one of formulae 1 to 12 may take the form of a trimer by binding with each other.

The polypeptide according to the first and the second aspect of the invention may be used for regulating the apoptosis induced in a living body.

For example, the polypeptide of the present invention which typically has an amino acid sequence defined by any one of formulae 1 to 12, and which is capable of binding with the Fas antigen to induce the apoptosis may be used for treating a cancer that have acquired carcinostatic resistance. Alternatively, the polypeptide of the present invention may be used for treating an early stage AIDS by inducing apoptosis of the HIV infected cells. Such treatments should constitute a new series treatments in the field of medicine.

Of the polypeptides according to the second aspect of the present invention, those which are capable of binding with the Fas antigen, but incapable of inducing the apoptosis, may be used for preventing the apoptosis of cells such as hepatocytes to thereby prevent a rapid decrease in the number of cells that constitute the organs critical for the patients such as liver, and hence, to prevent a rapid dysfunction of such organs, for example, in the case of hepatitis.

The polypeptides of the present invention may produced into medicaments in the form of, for example, an injection, a tablet, a capsule, a suppository, a spray, an ointment, a cataplam, or eye drops, in accordance with any of the conventional methods used for producing polypeptide-containing medicaments. For example, a medicament containing the polypeptide of the present invention as its effective ingredient in the form of an injection may be prepared by filling an ampul with a solution of the polypeptide that has been prepared under aseptic conditions, and lyophilizing the solution. The injection may additionally contain pharmaceutically acceptable additives such as a stabilizer. The thus prepared injection can be dissolved in distilled water of injection purpose before the intravenous or topical administration. Of the polypeptides according to the present invention, those which are most suitable for use as an effective ingredient in a medicament are the polypeptides having a low antigenicity for human such as the polypeptides containing the amino acid sequence defined by any one of formulae 1 to 4 or a fragment thereof, and in particular, those defined by formulae 1 and 4, or a fragment thereof.

The novel polypeptide of the present invention can be used by setting its administration method and dose depending on the age and sex of each patient and the kind and degree of each disease. In other words, it may be used in a dose which is effective in controlling apoptosis and hence in improving morbid states, by selecting a proper route of administration from oral administration and parenteral administration such as inhalation, percutaneous absorption, ophthalmic administration, vaginal administration, intraarticular injection, rectal administration, intravenous injection, topical application, intramuscular injection, subcutaneous injection, intraperitoneal administration and the like.

Also, the polypeptides according to the first or the second aspect of the invention may be used for preparing an antibody by immunizing an animal such as rabbit with the polypeptide of the present invention. Preparation of the antibody will be set forth in the description of the ninth aspect of the present invention. The resulting antibody may be used for staining tissues or cells, or for preparing an affinity column adapted for use in purifying the polypeptide of the present invention.

Next, the DNA according to the third aspect of the present invention is described.

In the description of the present invention, the term, "a DNA containing (or including) the nucleotide sequence defined by formula Y (or SEQ ID NO: Y)" designates a DNA having the nucleotide sequence defined by formula Y (or SEQ ID NO: Y) optionally having at least one nucleotide added on one or both of its 3' and 5' ends. The nucleotide added is not limited to any particular type so long as such addition of the nucleotide does not result in a frame shift. Exemplary sequences added include a linker sequence, termination codon sequence, a nucleotide sequences coding for signal peptide or other polypeptide, a sequence added in the production of a DNA probe for the purpose of increasing the detection sensitivity. The term, "DNA having the nucleotide sequence defined by formula Y (or SEQ ID NO: Y)." designates the DNA substantially represented by the nucleotide sequence defined by formula Y (or SEQ ID NO: Y).

The novel DNA of the third aspect of the present invention includes whole or a part of DNA which codes Fas ligand.

The novel DNA of the third aspect of the present invention is characterized in that it contains a nucleotide sequence which encodes the novel polypeptide of the first or the second aspect of the present invention

That is, the novel DNA of the present invention preferably contains a nucleotide sequence which encodes at least a part of any one of the amino acid sequences of the aforementioned formulae 1 to 12 (SEQ ID NO: 1 to 12).

15

Since it is known that 1 to 6 amino acid-encoding DNA triplets are present for each amino acid, the nucleotide sequence which encodes any one of the amino acid sequences of the aforementioned formulae 1 to 12 is not limited to one kind. In consequence, all DNA fragments comprising any kind of sequence are included in the novel DNA fragment of the present invention, provided that they contain a nucleotide sequence which encodes at least a part of any one of the amino acid sequences of the aforementioned formulae 1 to 12.

More preferably, the novel DNA fragment of the present invention is a fragment which contains at least a part of a nucleotide sequence represented by any one of the formulae 13 to 24 disclosed (SEQ ID NOS: 13 to 24).

The nucleotide sequences represented by the formulae 16, 20, and 24 encode the amino acid sequences represented by the formulae 4, 8, and 12, respectively. The nucleotide sequences represented by the formulae 15, 19, and 23 encode the amino acid sequences represented by the formulae 3, 7, and 11, respectively which are the extracellular regions of human, rat and mouse Fas ligand represented by the amino acid sequences of the formulae 4, 8, and 12, respectively. The nucleotide sequences represented by the formulae 13, 14, 17, 18, 21, and 22 encode the amino acid sequences represented by the formulae 1, 2, 5, 6, 9, and 10 which are shorter amino acid sequences than that of the polypeptides of the extracellular regions of human, rat and mouse Fas ligand.

The novel DNA fragment of the present invention may be either cDNA or chromosomal DNA, provided that it includes nucleotide sequences which encodes the novel polypeptide of the first and the second aspects of the present invention. As an example of such a type of chromosomal DNA, a nucleotide sequence of chromosomal DNA which contains a part of the aforementioned nucleotide sequence of formula 13 or 16 is shown in Figs. 16 to 18. It is desirable however that the novel DNA fragment of the present invention is cDNA, because it can be handled easily in carrying out genetic engineering techniques, such as the easiness to introduce it into a vector.

The DNA of the present invention is useful to produce the novel polypeptide of the first or the second aspect of the present invention by the recombinant DNA technique. The DNA of the present invention can be inserted into the vector containing an appropriate nucleotide sequence for expressing the polypeptides of the present invention such as promoter sequence, then, the thus obtained vector may be used to transformation of an appropriate host cell to produce the polypeptide of the first or the second aspect of the present invention. The polypeptide can be recovered from the transformant or the culture supernatant thereof.

As will be described in Examples, Fas ligand, namely, the polypeptides having the activity inducing apoptosis can be obtained from the culture supernatant of the transformant transformed with a recombinant DNA molecule which contain the DNA having the sequence represented by the formulae 16, 20 and 24.

The DNA having the nucleotide sequences represented by the formulae 13, 14, 15, 17, 18, 19, 21, 22, 23 are useful to obtain low molecular Fas ligands. The DNAs code the amino acid sequences represented by the formulae 1, 2, 3, 5, 6, 7, 9, 10, 11 which are the amino acid sequences of a part or whole the extracellular region of Fas ligand. When the DNA is bound to the downstream of a nucleotide sequence encoding an appropriate signal peptide to be expressed by a transformant the polypeptide of the present invention coded by the DNA can be obtained from the culture supernatant of the transformant.

As already described, it is more effective to recovering the polypeptides from the culture supernatant than from the lysate of cells. The DNA having the nucleotide sequences represented by the formulae 13, 14, 15, 17, 18, 21, 22, 23 are also useful, because it is low molecule and can be handled easily in carrying out by genetic engineering.

As mentioned above, the polypeptides derived from different animal species or different individuals of the same species may have different amino acid sequences, and hence, the DNAs coding for such polypeptides may have different nucleotide sequences. In spite of such variation in the sequence, the nucleotide sequences of the DNAs coding for proteins having an identical function are generally homologous with each other in spite of their different origin. In view of such situation, a DNA having the nucleotide sequence at least partly homologous to the nucleotide sequence defined in any one of formulae 13 to 24, namely, a DNA hybridizable with at least a part of the nucleotide sequence complimentary to the nucleotide sequence defined in any one of formulae 13 to 24 should code for a polypeptide having a function identical with the function of the polypeptide coded by the nucleotide sequence defined in any one of formulae 13 to 24. The term "hybridizable" used herein means that the sequence was hybridizable when the hybridization was carried out in accordance with a known method (see, for example, Sambrook, J. et al., Molecular Cloning, a Laboratory Manual 2nd ed., 1989, Cold Spring Harbor Laboratory, New York) by using at least a part of the sequence complimentary to the nucleotide sequence defined in any one of formulae 13 to 24 for the probe. In the Examples, hybridization is carried out by using a part of the nucleotide sequence complimentary to the nucleotide sequence of formula 19 for the probe.

As described above, the DNA hybridizable with the nucleotide sequence complimentary to the nucleotide sequence defined in any one of formulae 13 to 24 is included in the DNA according to the third aspect of the present invention. In particular, a DNA which is hybridizable with the nucleotide sequence complimentary to the nucleotide sequence defined in any one of formulae 13, 17 and 21, and which encodes the Fas ligand, is a preferred embodiment of the DNA according to the third aspect of the present invention.

The DNA according to the third aspect of the present invention may be a DNA fragment having a nucleotide sequence which is a part of the nucleotide sequence defined in any one of SEQ ID NOS: 27, 25 and 28. As demonstrated in the Examples, the nucleotide sequences of SEQ ID NOS: 27, 25 and 28 are containing the nucleotide sequences of the cDNAs obtained from the human, rat and mouse cDNA libraries in an effort to find the DNAs having the nucleotide sequences coding for the Fas ligand. The nucleotide sequence of SEQ ID NOS: 27, 25 and 28 include the nucleotide sequence of formulae 16, 20 and 24, respectively, within their sequences.

The nucleotide sequence which is a part of the nucleotide sequence defined in any one of SEQ ID NOS: 27, 25 and 28 may comprise any desired part of the nucleotide sequence. Such fragment is not limited in its length, and may comprise, for example, a part of the nucleotide sequence of formula 16, 20 or 24, or a part of the non-coding region on 5' or 3' end of the nucleotide sequence.

The DNA as described above may be used for the prove in cloning the DNA coding for the apoptosis-inducing polypeptides, or as a primer in PCR.

The DNA as described above may also be used for a diagnostic DNA prove in detecting or quantitating the polypeptides according to the first or the second aspect of the present invention in the tissue of cells after labeling the DNA with an enzyme such as horse radish peroxidase (HRPO), a radioisotope, a fluorescent substance, or a chemiluminescent substance.

The DNA according to the third aspect of the present invention is not limited for its production process or source. In other words, the DNA according to the third aspect of the present invention may be a DNA chemically synthesized on the bases of any one of formulae 13 to 24 (SEQ ID NOS: 13 to 24) or SEQ ID NOS: 27, 25 and 28; or a DNA cloned from an appropriate DNA library.

The chemical synthesis of the DNA according to the present invention may be conducted by dividing the desired nucleotide sequence into regions each comprising about 20 nucleotides by referring to any one of formulae 13 to 24 and SEQ ID NOS: 27, 25 and 28; synthesizing the fragments corresponding to such regions with a DNA chemical synthesizer (for example, 394, Perkin-Elmer Japan K.K.); annealing the thus synthesized fragments after optional phosphorylation of the 5' end of the fragments; and ligating the thus annealed fragments to produce the desired DNA.

Isolation of the novel DNA of the present invention from a DNA library may be effected for example by a method in which an appropriate genomic DNA library or cDNA library is screened by means of a hybridization or immunoscreening using antibody, the thus screened clones having the DNA fragment of interest is cultured and then the DNA fragment is cut out using restriction enzymes and the like.

Hybridization can be effected by labeling a DNA fragment containing entire portion or a part of the nucleotide sequence of any one of the aforementioned formulae 13 to 24 and SEQ ID NOS: 27, 25, and 28

with ³²P or the like and then carrying out screening from any cDNA library using the labeled DNA fragment as a probe in accordance with known methods (for example, see Maniatis T. *et al., Molecular Cloning, a Laboratory Manual*, Cold Spring Harbor Laboratory, New York, 1982).

With regard to the antibody to be used in the immunoscreening, the antibody of the ninth aspect of the present invention which will be described later may be used.

The novel DNA of the present invention can also be obtained by PCR (polymerase chain reaction) using a genomic DNA library or a cDNA library as a template.

That is, the novel DNA of the present invention can be obtained by preparing sense and antisense primers based on any one of the nucleotide sequences of the aforementioned formulae 13 to 24 or SEQ ID NOS: 27, 25, and 28, and carrying out PCR using any DNA library in accordance with any known method (e.g. see Michael A.I. et al., PCR Protocols, a Guide to Methods and Applications, Academic Press, 1990).

Any type of DNA library can be used in the aforementioned various methods, provided that it contains the DNA fragment of the present invention, such as a commercially available DNA library or a cDNA library prepared from appropriate cells which contain the DNA and in suitable to obtain a cDNA library in accordance with a known method (c.f. Sambrook J. et al., Molecular Cloning, a Laboratory Manual, 2nd. ed., Cold Spring Harbor Laboratory, New York, 1989).

When a DNA nucleotide sequence is provided, an RNA sequence and the complementary DNA and RNA sequence are determined automatically. In consequence, an RNA sequence which corresponds to the DNA fragment of the third aspect of the present invention and a DNA and RNA fragment having a sequence complementary to the DNA fragment of the third aspect of the present invention are also provided by the disclosure of the present invention.

The DNA of the third aspect of the present invention may be single-stranded or may form a doublestranded or triple-stranded chain through the binding of a DNA or RNA fragment.

The novel DNA may also be labeled with an enzyme such as horseradish peroxidase (HRPO), a radioactive isotope, a fluorescent material, a chemiluminescent material or the like.

25

The novel DNA of the present invention can be used for the large scale production of the novel polypeptide of the first and the second aspects of the present invention. An example of the process for the production of the novel polypeptide of the present invention making use of the novel DNA will be described later in relation to the seventh aspect of the present invention. The novel DNA can also be used for the inspection of the expression condition of the novel protein of the first or the second aspect of the present invention in tissues, by labeling the fragment with the enzyme or the like as described above. By confirming expression quantity of the novel protein of the first or the second aspect of the present invention in cells making use of the novel DNA, cells and culture condition of the cells suitable for use in the production of the novel protein of the first or the second aspect of the present invention can be determined.

Also, the novel DNA of the present invention can be used in the gene therapy of diseases in which the mechanism of apoptosis is deleted hereditarily, such as autoimmune diseases and the like, by introducing the DNA fragment into cells of the living body.

In addition, it is possible also to develop an antisense pharmaceutical preparation based on the nucleotide sequence contained in the novel DNA of the present invention for use in the regulation of the expression of Fas ligand in the living body. That is, it is possible to regulate expression of Fas ligand making use of an oligonucleotide or a derivative thereof which contains a sequence complementary to any one of the nucleotide sequences of the aforementioned formulae 13 to 24 or SEQ ID NOS: 25, 27 and 28. Techniques for the production of antisense pharmaceutical preparations will be described later in detail in relation to the tenth aspect of the present invention.

Next, a recombinant DNA molecule as a fourth aspect of the present invention is described.

The recombinant DNA molecule of the fourth aspect of the present invention is a recombinant DNA molecule which is characterized in that it contains the aforementioned novel DNA of the third aspect of the present invention. The recombinant DNA molecule of the present invention may have any form such as circular, linear or the like structure. Also, the recombinant DNA molecule of the present invention may be used for any purpose. For example, it may be used when the novel polypeptide of the first and the second aspects of the present invention is produced or when the novel DNA of the third aspect of the present invention is amplified and produced in a large quantity.

If necessary, the recombinant DNA molecule of the fourth aspect of the present invention may contain other nucleotide sequence in addition to the novel DNA of the third aspect of the present invention. Examples of the "other nucleotide sequence" as used herein include an enhancer nucleotide sequence, a promoter nucleotide sequence, a ribosome binding sequence, a nucleotide sequence which is used for the purpose of amplifying copy numbers, a nucleotide sequence which encodes a signal peptide, a nucleotide

sequence which encodes other polypeptide, adenylation site, a splicing sequence, a replication origin and a nucleotide sequence of a gene to be used as a selection marker. The necessity of these nucleotide sequences is determined depending on the use of the recombinant DNA molecule. Preferably, however, the recombinant DNA molecule of the present invention may contain at least a replication origin and a marker gene in addition to the novel DNA of the third aspect of the present invention. Examples of the marker gene include ampicillin resistant gene, kanamycin resistant gene, neomycin resistant gene, thymidine kinase gene and the like.

A preferred example of the recombinant DNA molecule is a molecule which can transform *E. coli* so that the novel protein of the first and the second aspects of the present invention can be expressed in the host cells. It is preferable therefore that the recombinant DNA molecule of the present invention contains at least an *E. coli* replication origin, a marker gene and a promoter sequence which functions in *E. coli* cells in addition to the novel DNA fragment of the third aspect of the present invention. Also, in addition to these sequences, it may preferably contain a sequence which encodes a signal peptide. Ideal examples of the promoter sequence which functions in *E. coli* cells include *trp* promoter and *lac* promoter, and ideal examples of the signal peptide which functions in *E. coli* cells include the *E. coli* alkaline phosphatase signal peptide.

Another preferred example of the recombinant DNA molecule is a molecule which can transform eucaryotic cells such as yeast cells, insect cells, animal cells and the like so that the novel polypeptide of the present invention can be expressed in the host cells. It is preferable therefore that the recombinant DNA molecule of the present invention contains at least a marker gene, adenylation site and a promoter sequence which functions in eucaryotic cells in addition to the novel DNA fragment of the third aspect of the present invention. Ideal examples of the promoter which functions in eucaryotic cells include alcohol oxidase (AOX) 1 promoter which functions in yeast, polyhedrin promoter which functions in insect cells and SV40 promoter, SR_{α} promoter and human elongation factor I_{α} (EF- I_{α}) promoter which function in animal cells. More preferably, the recombinant DNA molecule may further contain an *E. coli* replication origin.

The recombinant DNA molecule of the fourth aspect of the present invention can be obtained by introducing the novel DNA fragment of the third aspect of the present invention into an optional vector. In this step, the novel DNA may be introduced with optional sequence into a vector as occasion demand. Alternatively, the recombinant DNA molecule of the present invention can be obtained by carrying out ligation of the novel DNA fragment of the third aspect of the present invention with a DNA fragment which contains an optional nucleotide sequence. Introduction of a DNA fragment into a vector can be made in accordance with any known method (e.g., see Sambrook J. et al., Molecular Cloning, a Laboratory Manual, 2nd. ed., Cold Spring Harbor Laboratory, New York, 1989). That is, a DNA fragment and a vector are respectively digested with appropriate restriction enzymes and the resulting fragments are subjected to ligation using DNA ligase. The vector may be any of plasmid vectors, phage vectors, virus vectors and the like. For example, it may be selected optionally from pUC118, pBR322, pSV2-dhfr, pBluescript II, PHIL-S1, λZap II, λqt10, pAc700, YRP17, pEF-BOS, pEFN-II and the like.

Next, a transformant as a fifth aspect of the present invention is described.

The transformant of the fifth aspect of the present invention is characterized in that it is transformed with the novel DNA fragment of the third aspect of the present invention. In other words, the transformant of the fifth aspect of the present invention is characterized in that it is transformed by introducing the novel DNA fragment of the third aspect of the present invention directly into appropriate cells or microorganism used as the host.

Introduction of the novel DNA fragment of the third aspect of the present invention into host cells can be effected by any of the known methods such as electroporation, protoplast method, alkali metal method, calcium phosphate precipitation, DEAE dextran method, microinjection, and a method in which virus particles are used [see Jikken Igaku (Experimental Medicine) supplement, Idenshi Kogaku (Gene engineering) Hand Book, March 20, 1991, Yohdo-sha).

The transformant of the present invention can be used for the purpose of producing the novel DNA fragment of the third aspect of the present invention in a large quantity. In addition, when the novel DNA of the third aspect of the present invention is integrated into downstream of an appropriate promoter in the host cells, the resulting transformant produces the novel polypeptide of the first and the second aspects of the present invention. In consequence, such a transformant can be used for the purpose of producing the novel polypeptide of present invention.

Next, another transformant as a sixth aspect of the present invention is described.

55

The transformant of the sixth aspect of the present invention is characterized in that it is transformed by introducing the recombinant DNA molecule of the fourth aspect of the present invention into cells or microorganism used as the host. In this case, it is necessary to select a recombinant DNA molecule which

suits the host. In other words, said recombinant DNA molecule should be obtained by introducing the novel DNA fragment of the third aspect of the present invention into a vector which suits the host. Also, said recombinant DNA molecule should have a promoter, a nucleotide sequence encoding a signal peptide, a marker gene and the like which suit the host. Examples of preferred combination of vectors and hosts include pUC118 with E. coli, pEF-BOS with COS cells or CHO cells, Yac with yeast and AcNPV with Sf cells [see Jikken Igaku (Experimental Medicine) supplement, Idenshi Kogaku (Gene engineering) Hand Book, March 20, 1991, Yohdo-sha).

Similar to the case of the preparation of the transformant of the fifth aspect of the present invention, introduction of the recombinant DNA molecule of the fourth aspect of the present invention into host cells can be effected by any of the known methods such as electroporation, protoplast method, alkali metal method, calcium phosphate precipitation, DEAE dextran method, microinjection, and a method in which virus particles are used [see Jikken Igaku (Experimental Medicine) supplement, Idenshi Kogaku (Gene engineering) Hand Book, March 20, 1991, Yohdo-sha).

The host to be transformed may be either procaryotic or eucaryotic cells. Typical examples of procaryotic cells include those of *Escherichia coli* and *Bacillus subtilis*. Typical examples of eucaryotic cells include mammalian cells such as CHO cells, HeLa cells, COS cells, Namalwa cells and the like, insect cells such as Sf cells and the like and yeast cells.

The transformant of the sixth aspect of the present invention may be obtained by transforming any type of cells, but preferably *E. coli*, mammalian cells or yeast. As mammalian cells, a *dhfr* deletion mutant of CHO cells is preferred because of its ability to increase gene copy numbers. With regard to yeast cells, a strain belonging to the genus *Pichia* is preferred in view of the high expression and secretion quantity of exogenous polypeptide.

The transformant of the sixth aspect of the present invention can be used for the purpose of obtaining the novel DNA fragment of the third aspect of the present invention in a large quantity and producing the novel polypeptide of the first and the second aspects of the present invention.

Said transformant may be used for any purpose, but preferably for the production of the novel polypeptide of the present invention.

In other words, a preferred transformant of the present invention is a transfromant which produce the novel polypeptide of the first or the second aspect of the present invention.

More preferably, the transformant of the present invention is a transformant which secretes the novel polypeptide into culture medium.

The transformant capable to express and secrete the polypeptide of the present invention can be obtained by transforming host cells with a recombinant DNA molecule which comprises the novel DNA of the third aspect of the present invention and a signal peptide-encoding sequence linked to the 5'-end of the DNA fragment.

Preferred example of the transformant of the present invention is an *E. coli* strain transformed with a recombinant DNA molecule which contains, in a DNA molecule capable of functioning as a vector, at least a replication origin, a promoter that functions in *E. coli* cells, a marker gene, a nucleotide sequence that encodes a signal peptide such as of *E. coli* alkaline phosphatase or the like and the novel DNA fragment of the third aspect of the present invention. Another preferred example of the transformant of the present invention is a mammalian cell strain transformed with a recombinant DNA molecule which contains, in a DNA molecule capable of functioning as a vector, at least a marker gene, adenylation site, a promoter that functions in mammalian cells and the novel DNA fragment of the third aspect of the present invention. Also preferred as the transformant of the present invention is a strain of yeast belonging to the genus *Pichia* transformed with a recombinant DNA molecule which contains, in a DNA molecule capable of functioning as a vector, at least an AOX1 promoter, a marker gene and the novel DNA fragment of the third aspect of the present invention.

Next, a production process as a seventh aspect of the present invention is described.

The production process of the seventh aspect of the present invention is a process for the production of the novel polypeptide of the first aspect of the present invention, which is characterized in that the transformant of the fifth or sixth aspect of the present invention is used. Method for the preparation of the transformant was already described.

According to the production process, the transformant of the fifth or sixth aspect of the present invention is firstly cultured. In this step, amplification and expression-induction of the gene of interest are carried out as occasion demands. Next, the resulting culture mixture is recovered to purify the novel polypeptide of the present invention by carrying out concentration, solubilization, dialysis, various types of chromatography and the like.

Host to be transformed for use in this production process are not particularly limited. However, a preferred transformant may be obtained by transforming host selected from mammalian cells such as CHO cells and the like, yeast and *E. coli*.

Culturing of the transformant can be carried out in the usual way with reference to various published papers and books (e.g., "Biseibutsu Jikken-ho" (Microbial Experiments), Japanese Biochemical Society, Tokyo Kagaku Dojin, 1992). Methods and necessity for the amplification and expression-induction of the gene vary depending on the kind of host and the promoter to be used. For example, the induction may be effected with 3b-indoleacrylic acid when the promoter is *trp* promoter, with dexamethasone in the case of MMTV promoter or with methanol in the case of AOX1 promoter.

On the other hand, when the host is $dhfr^-$ CHO cells and the vector to be used in the transformation containing $dhfr^+$, the gene of interest can be amplified by treating the transformant with methotrexate.

Examples of the culturing and expression induction are shown below when *E. coli*, CHO cells or a yeast strain belonging to the genus *Pichia* are used as the host of each transformant.

In the case of an *E. coli* strain transformed with a recombinant DNA molecule which contains *trp* promoter, cells are pre-cultured in L-broth, inoculated into M9-CA medium in a 1/50 volume and then cultured at 37 °C. When the OD₅₅₀ value of the medium reaches 1 to 4 several hours after commencement of the culturing (namely logarithmic growth phase), 3b-indoleacrylic acid is added to a final concentration of 10 μg/ml to effect expression-induction. By continuing the culturing for about 1 to 2 days, a culture mixture containing the polypeptide of interest is obtained.

When a *Pichia* strain transformed with a recombinant DNA molecule which contains AOX1 promoter is used, the yeast cells are pre-cultured in BMGY medium for about 2 days and, after medium exchange, methanol is added to effect expression induction. By continuing the culturing at 30 °C for about 2 days, a culture mixture containing the polypeptide of interest is obtained.

In the case of a transformant of mammalian cells such as CHO cells or the like transformed with an expression plasmid which contains an elongation factor promoter, the transformant is cultured in D-MEM (Dulbecco's modified Eagle's Medium) containing 10% fetal bovine serum. The cells are inoculated in a density of about 5 x 10⁴ cells/ml and cultured at 37 °C in an atmosphere of 5% CO₂/95% air. When the cells become confluent generally after 2 to 3 days of the culturing, the medium is exchanged with serum-free DMEM. By continuing the culturing for 2 to 3 days, a culture mixture containing the polypeptide of interest is obtained. When productivity of the polypeptide of interest is low, it is possible to increase the productivity in the aforementioned manner by using dhfr⁻ CHO cells and amplifying the gene with methotrexate.

According to the seventh aspect of the present invention, the term "culture mixture" means a culture supernatant or a cell. That is, when the transformant secretes the polypeptide of interest into the extracellular milieu, the novel polypeptide of interest of the first and second aspects of the present invention is recovered and purified from the culture supernatant.

On the other hand, when the novel polypeptide is accumulated in the host cells, the cells are disrupted by lysozyme treatment, surfactant treatment, freezing-thawing, pressurization or the like means and subjected to centrifugation to recover the supernatant fluid from which unnecessary cell debris and the like are subsequently removed by filtration or the like means, the supernatant fluid is used as the material for the purification of the novel polypeptide of the first aspect of the present invention. When the transformant to be used is *E. coli* and the produced novel polypeptide is accumulated in the periplasmic space of the cells, the polypeptide of interest can be purified with reference to, for example, the procedure of Willsky *et al.* (*J. Bacteriol.*, vol. 127, pp. 595 - 609, 1976).

The novel polypeptide of the first and the second aspects of the present invention can be purified from the culture mixture by optionally selecting appropriate techniques commonly used for the purification of polypeptide, such as salting out, ultrafiltration, isoelectric precipitation, gel filtration, electrophoresis, ion exchange chromatography, various types of affinity chromatography such as hydrophobic chromatography, antibody chromatography and the like, chromatofocusing and reverse phase chromatography, as well as an HPLC system and the like as occasion demands. These purification steps may be employed in any appropriate order. A preferred example of the purification process will be described later in relation to the eighth aspect of the present invention.

45

According to the production process of the present invention, the novel polypeptide of the present invention may be produced by the transformant in the form of a fusion polypeptide with other polypeptide. For example, a high productivity can be expected from a generally used process in which a DNA fragment coding for a polypeptide of interest is linked to a downstream site of another DNA fragment which encodes $E.\ coli\ \beta$ -galactosidase and the polypeptide of interest is expressed as a fusion polypeptide with β -galactosidase.

When the novel polypeptide of the present invention is expressed in the form of a fusion polypeptide with other polypeptide, it is necessary to insert an additional step between certain steps of the purification process, in order to cut out the novel polypeptide by treating the fusion polypeptide with a chemical substance such as cyanogen bromide or the like or an enzyme such as protease or the like.

In addition, when the transformant to be used is an *E. coli* strain and the novel polypeptide is produced in the form of inclusion body which is an insoluble protein, an appropriate step of the purification process may be followed by a procedure in which the inclusion body is subjected to solubilization, denaturation and refolding (Thomas E. and Creighton J., Molecular Biology, vol. 87, pp. 563 - 577, 1974).

Illustratively, the transformants are firstly disrupted and subjected to centrifugation to recover the resulting pellet. Next, to the pellet is added a solubilization buffer containing appropriate amounts of urea or guanidine hydrochloride, a surface active agent, reduced type glutathione and oxidized type glutathione (for example, a buffer containing 5 M guanidine hydrochloride, 0.005% Tween 80, 50 mM tris hydrochloride (pH 8.0), 5 mM EDTA, 2 mM reduced type glutathione and 0.02 M oxidized type glutathione), followed by the addition of 2-mercaptoethanol to effect denaturation. Thereafter, refolding is effected by dialyzing the resulting solution against the above solubilization buffer from which guanidine hydrochloride is eliminated. When expressed as a fusion polypeptide, the unnecessary polypeptide portion is cut and removed after these treatment using a chemical substance such as cyanogen bromide or the like or an enzyme such as protease or the like, and the thus freed novel polypeptide of interest is subsequently subjected to an appropriate chromatography.

Next, a eighth aspect of the present invention is described.

The eighth aspect of the present invention is a process for the purification of the novel polypeptide of the first and the second aspects of the present invention from a sample which contains the novel polypeptide of the first aspect of the present invention, which is characterized in that at least one step selected from the following purification steps is carried out:

(1) an affinity chromatography making use of a Fas antigen, and

25

55

(2) an affinity chromatography making use of an antibody which recognizes the novel polypeptide of the first or the second aspect of the present invention.

The purification process of the present invention may be effected by either one of the above steps (1) and (2) or by both of them. Alternatively, it may be effected by a combination of other purification method with at least one of the above steps (1) and (2). Preferably, however, either one of the above steps (1) and (2) or both of the steps may be carried out in an optional order before or after a generally used method for the purification of protein.

For example, the novel polypeptide of the first or the second aspect of the present invention can be obtained with a high purity by employing a chromatography in which a lectin-adsorbed carrier is used, in addition to either one of the above steps (1) or (2).

The term "a sample which contains the novel polypeptide of the first aspect of the present invention" means any sample provided that it contains said novel polypeptide. For example, it may be a culture supernatant of cells, a cell lysate or a body fluid such as urine, blood or the like.

In carrying out the affinity chromatography of the above step (1), it is necessary to adsorb the Fas antigen to an appropriate carrier. The Fas antigen to be used may be of any animal origin provided that it binds to the polypeptide of interest. However, it is preferable to use human Fas antigen when the polypeptide of interest to be purified contains at least a part of the amino acid sequence of the aforementioned formula 1 to 4, or rat Fas antigen or mouse Fas antigen when the polypeptide of interest contains at least a part of the amino acid sequence of the aforementioned formula 5 to 8, or mouse Fas antigen when the polypeptide of interest contains at least a part of the amino acid sequence of the aforementioned formula 9 to 12.

The carrier to which the Fas antigen is adsorbed is not particularly limited. When the Fas antigen is bound to a carrier, the Fas antigen is bound to the carrier directly or via a spacer. Alternatively, the Fas antigen may be bound to a carrier indirectly, by preparing the Fas antigen as a fusion polypeptide with other polypeptide and binding a portion of the fusion polypeptide other than the Fas antigen moiety to a bondable carrier. For example, a Fas antigen-adsorbed carrier to be used in said affinity chromatography can be obtained easily, by preparing the Fas antigen as a fusion polypeptide with the constant domain of immunoglobulin and adsorbing the fusion polypeptide to a protein A-adsorbed carrier packed in a column making use of the property of immunoglobulin to bind to protein A.

In order to carry out the affinity chromatography of the above step (2), a novel antibody of the ninth aspect of the present invention, which will be described later, may be used. That is, said novel antibody is allowed to bind to a proper carrier such as agarose or the like directly or via a spacer, and the resulting carrier is packed in a column for use in the affinity chromatography.

In this instance, preferred examples of the aforementioned lectin-adsorbed carrier include ConA-adsorbed carriers. Since products in which ConA is adsorbed to an agarose carrier and the like are commercially available, it may be convenient to use one of these products by optionally selecting therefrom.

The affinity chromatography of the above step (1) or (2) or the affinity chromatography in which a lectinadsorbed carrier is used may be carried out by optionally selecting an eluting solution from solutions to be used in the polypeptide purification and confirming the amount of the polypeptide of interest in the eluted fractions. The presence of the novel polypeptide of the first or the second aspect of the present invention can be confirmed by measuring cytotoxic activity on Fas antigen-expressing cells or by means of EIA making use of an antibody which recognizes the novel polypeptide of the first or the second aspect of the present invention. The antibody which recognizes the novel polypeptide of the first or the second aspect of the present invention is described in the following ninth aspect of the present invention.

Next, a novel antibody as an ninth aspect of the present invention is described.

The novel antibody of the ninth aspect of the present invention is characterized in that it binds to the novel polypeptide of the first or the second aspect of the present invention.

The novel antibody of the ninth aspect of the present invention may be either a monoclonal antibody or a polycional antibody, provided that it binds to the novel polypeptide of the first or the second aspect of the present invention.

Antibody, namely immunoglobulin, has a structure which comprises H and L chains and is divided into 5 classes (IgG, IgA, IgM, IgD and IgE) depending on their physico-chemical and immunological properties. Of these classes, IgG and IgA are further divided into subclasses depending on the types of H chains. The novel antibody of the present invention may belong to any of these classes and subclasses. In addition, immunoglobulin is split into F(ab')₂ and Fc' fragments when hydrolyzed with pepsin, or into Fab and Fc fragments when hydrolyzed with papain. The novel antibody of the present invention may be either a complete antibody molecule or a partial fragment thereof, provided that it binds to the novel polypeptide of the first aspect of the present invention. Also, the antibody of the present invention may be in the form of a chimera antibody.

The novel antibody of the present invention, either as a polyclonal antibody or a monoclonal antibody, can be obtained with reference to published methods [see for example, $M\acute{e}n-eki$ Jikken Sosa-ho - (Procedures for Immunological Experiments), The Japanese Society for Immunology]. The following briefly describes the method.

In order to obtain the novel antibody, the novel polypeptide of the first aspect of the present invention is inoculated as an immunizing antigen into an animal, if necessary, with an appropriate adjuvant such as Freund's complete adjuvant (FCA) or Freund's incomplete adjuvant (FIA) or the like, followed, if necessary, by the booster at 2 to 4 week intervals. After completion of the booster, blood is collected to obtain antiserum. The novel polypeptide of the present invention to be used as the antigen may be obtained by any method, provided that it has such a purity that it can be used for the production of the antibody.

When the novel polypeptide used as immunizing antigen is low molecular one, such as a polypeptide composed of about 10 to 20 amino acid residues, the thus polypeptide can be used after binding it to a carrier such as keyhole limpet hemocyanin (KLH) or the like. The animal to be immunized with the novel polypeptide is not particularly limited, but it may preferably be selected from animal species capable of producing the antibody of interest, such as rat, mouse, rabbit, sheep, horse, domestic fowl, goat, pig, cattle and the like which are generally used in immunological experiments.

The polyclonal antibody can be obtained by purifying the thus obtained antiserum through optional combination of known purification methods such as salting out, ion exchange chromatography, affinity chromatography and the like.

The monoclonal antibody can be obtained in the following manner. That is, antibody producing cells such as splenocytes, lymphocytes or the like are collected from the immunized animal and fused with myeloma cells or the like to make them into hybridoma cells by a known method in which polyethylene glycol, Sendai virus, electric pulse or the like is used. Thereafter, a clone capable of producing an antibody which binds to the novel protein of the present invention is selected and cultured, and the monoclonal antibody of interest is purified from the resulting culture supernatant. The purification may be effected through optional combination of known purification methods such as salting out, ion exchange chromatography, affinity chromatography and the like.

The novel antibody can also be obtained by means of genetic engineering techniques. That is, mRNA is isolated from splenocytes or lymphocytes of an animal which is immunized with the novel polypeptide of the first or the second aspect of the present invention or from a hybridoma capable of producing a monoclonal antibody which is specific for the novel polypeptide of the first aspect of the present invention,

and a cDNA library is prepared using the thus isolated mRNA. Thereafter, a clone capable of producing an antibody which reacts with the antigen is screened from the cDNA library and cultured to obtain a culture supernatant from which the antibody of interest is purified through combination of known purification methods.

The novel antibody of the present invention may have an activity to modify the function of the Fas ligand on cells. Among antibodies which have the activity to modify the function of the Fas ligand on cells, most preferred is an antibody which has an activity to inhibit Fas ligand-induced apoptosis. Such an antibody may inhibit the Fas ligand-induced apoptosis completely or partially.

In order to obtain an antibody which has the activity to inhibit the Fas ligand-induced apoptosis, sera obtained during the aforementioned polyclonal or monoclonal antibody production process or culture supernatants of the aforementioned hybridoma cells are screened by subjecting them to an assay system such as an *in vitro* assay system in which Fas ligand or Fas ligand-expressing cells and Fas antigenexpressing cells are used. Thereafter, the antibody of interest is purified from a serum sample or a culture supernatant thus obtained as the result of the screening, through combination of known purification methods. A preferred example of the screening method in which Fas ligand or Fas ligand-expressing cells and Fas antigen-expressing cells are used will be described later in relation to the eleventh aspect of the present invention.

The antibody capable of inhibiting the Fas ligand-induced apoptosis completely or partially can be used in the regulation of apoptosis in the living body. For example, said antibody can be used as a pharmaceutical preparation for the treatment of diseases in which apoptosis of tissues and cells takes part, such as degradation of joint tissues in rheumatism, self tissue degradation in systemic lupus erythematosus (SLE), diabetes mellitus, influenza, AIDS, hepatitis and the like.

Next, a tenth aspect of the present invention is described.

35

The tenth aspect of the present invention is an oligonucleotide or a derivative thereof which contains a nucleotide sequence complementary to a part of the gene of a Fas ligand or a part of mRNA for a Fas ligand. Said oligonucleotide or a derivative thereof may contain, as its nucleotide sequence, either only said complementary nucleotide sequence or other bases and nucleotide sequences such as ribozyme sequence and the like in addition to the complementary nucleotide sequence.

The term "gene of a Fas ligand" as used herein means a gene which contains Fas ligand-encoding DNA, including not only a Fas ligand-encoding region but also its regulatory region. The regulatory region means both of which are located upstream and downstream of the Fas ligand-encoding region. The term "mRNA for the Fas ligand" means a mRNA which contains a Fas ligand-encoding nucleotide sequence. Said mRNA also includes a mRNA molecule which contains not only the Fas ligand-encoding nucleotide sequence but also non-coding regions located upstream and downstream of the nucleotide sequence.

As shown in Figs. 16 to 18, the Fas ligand-encoding chromosomal DNA is composed of introns and exons. When a DNA fragment containing introns and exons is transcribed into mRNA, the introns and exons are firstly transcribed as such to form pre-mRNA. Thereafter, portions corresponding to the introns are eliminated by splicing to form mature mRNA in which only the exons are transcribed. The term "mRNA for the Fas ligand" as used herein means both pre-mRNA and mature mRNA.

The term "a part of the gene of a Fas ligand or a part of mRNA for the Fas ligand" as used herein means any part contained in the Fas ligand gene or mRNA for the Fas ligand, independent of their coding and non-coding regions and intron and exon sites.

According to the tenth aspect of the present invention, the "Fas ligand" may be of any animal origin, but it may preferably be obtained from human, rat or mouse. Human Fas ligand is particularly preferable when its application to diagnostic drugs and pharmaceutical preparations is taken into consideration.

A nucleotide sequence in and around the coding region of the human Fas ligand is shown in Figs. 16 to 18. Nucleotide sequences contained mature mRNAs for human Fas ligand, rat Fas ligand and mouse Fas ligand are obtained by changing T to U in the DNA sequences of the SEQ ID NOS: 27, 25 and 28, which respectively encode these ligands.

The term "complementary nucleotide sequence" as used herein means a nucleotide sequence which forms complementary base pairs base-specific for the nucleotide sequence of DNA or mRNA. It is known in general that the complementary base pairs are formed between C (cytosine) and G (guanine), T (thymine) and A (adenine) and U (uracil) and A (adenine). In consequence, a nucleotide sequence complementary to the human Fas ligand gene and nucleotide sequences complementary to the mature mRNAs for human Fas ligand, rat Fas ligand and mouse Fas ligand are respectively obtained by changing A to T, C to G, G to C and T to C, or A to U, C to G, G to C and T to A, of the nucleotide sequences shown in Figs. 16 to 18 and or the SEQ ID NOS: 31, 25 and 28. A DNA and RNA sequence complementary to the nucleotide sequence encoding the human Fas ligand of SEQ ID NO: 31 are shown by SEQ ID NOS: 29 and 30 respectively. In

this instance, the "complementary nucleotide sequence" includes not only those composed of C, G, A, T and U but also those which contain derivatives of these bases.

The oligonucleotide of the present invention includes every oligonucleotide composed of a plurality of nucleotides, each of which comprising bases, phosphoric acid and sugars. Typical examples are DNA and RNA.

The oligonucleotide derivative of the present invention includes every derivative whose stereochemical structure and function are analogous to the oligonucleotide. Examples of such derivatives include a derivative resulting from the binding of an exogenous substance to the 3'- or 5'-end of the oligonucleotide, a derivative resulting from the substitution or modification of at least one of the bases, sugar moieties and phosphate moieties of the oligonucleotide, a derivative resulting from the inclusion of a base, a sugar or a phosphoric acid moiety which does not exist in nature and a derivative which contains a backbone other than phosphodiester.

Preferably, the oligonucleotide or a derivative thereof of the tenth aspect of the present invention has a nucleotide sequence which is complementary to a part of the Fas ligand gene or a part of mRNA for the Fas ligand and hybridizes with such gene and mRNA.

The oligonucleotide or a derivative thereof which hybridizes with the Fas ligand gene or mRNA for the Fas ligand can be used as a diagnostic oligonucleotide probe for the examination of the presence and expressing condition of the Fas ligand gene in tissues and cells.

More preferably, the oligonucleotide or a derivative thereof of the present invention hybridizes with the Fas ligand gene or mRNA for the Fas ligand and has an activity to control expression of the Fas ligand.

A method for controlling expression of a protein making use of an oligonucleotide which contains a nucleotide sequence complementary to a DNA or mRNA that encodes the protein is a technique called antisense method which is now studied by many researchers. It is considered that an oligonucleotide having a complementary sequence controls expression of protein by exerting an influence upon the normal flow of the transfer of genetic information through its binding to a DNA or mRNA which bears the genetic information, wherein the binding occurs at any one of the steps for the (1) transcription from the gene to pre-mRNA, (2) processing of the pre-mRNA into mature mRNA, (3) passing of the mature mRNA through nuclear membrane and (4) translation into protein.

As described in the foregoing, the cause of the cell death in the case of AIDS and hepatitis is considered to be Fas antigen-mediated apoptosis. In consequence, a oligonucleotide or a derivative thereof capable of inhibiting expression of the Fas ligand can be used for the treatment of diseases in which Fas ligand-mediated apoptosis takes part, such as AIDS and hepatitis, as well as degradation of joint tissues in rheumatism, self tissue degradation in systemic lupus erythematosus (SLE), diabetes mellitus, influenza and the like.

On the other hand, another oligonucleotide or a derivative thereof capable of enhancing expression of the Fas ligand can be used for the removal of cells which are unnecessary for the living body, for example for the treatment of AIDS at an early stage of the infection and for the inhibition of abnormal growth of synovial membrane cells in rheumatism or growth of autoantigen-reactive T cells in autoimmune diseases. Thus, both of the Fas ligand expression inhibiting and enhancing oligonucleotides are useful in the field of medical care. Most preferably, however, the oligonucleotide or a derivative thereof of the present invention may have a function to inhibit expression of the Fas ligand.

The oligonucleotide or a derivative thereof of the present invention may hybridize with any part of the Fas ligand gene or mRNA. In general, it is considered that easy hybridization can be made when aimed at the loop moiety of stem loop-forming mRNA [Y. Shoji, *Rinsho Men-eki* (Clinical Immunology), vol. 25, pp. 1200 - 1206, 1993], namely in case of an oligonucleotide or a derivative thereof having a sequence complementary to the sequence of these region.

Also, oligonucleotides which bind to translation initiation codon area, ribosome binding site, capping site and splice site, namely oligonucleotides having sequences complementary to the sequences of these sites, are generally considered to have high expression inhibition effect [Gan to Kagaku Ryoho (Cancer and Chemotherapy), vol. 20, no. 13, pp. 1899 - 1907]. In consequence, a high expression inhibition effect can be expected from the oligonucleotide or a derivative thereof of the present invention when it can bind to the translation initiation codon area of the Fas ligand gene or mRNA, ribosome binding site, capping site or splice site, namely when it contains a sequence complementary to each of these sites.

When its application to diagnostic and pharmaceutical use is taken into consideration, the oligonucleotide and a derivative thereof of the present invention may preferably have a function to hybridize with the Fas ligand gene or mRNA in a specific manner.

In general, a nucleotide sequence containing 15 or more bases is considered to be a sequence having specificity (K. Yokoyama, *Protein, Nucleic acid and Enzyme*, vol. 38, pp. 754 - 765, 1994). In con-

sequence, specific binding to the Fas ligand gene or mRNA for Fas ligand can be expected from said oligonucleotide or a derivative thereof when it contains a nucleotide sequence which is complementary to the Fas ligand gene or mRNA for Fas ligand and composed of 15 or more bases.

On the other hand, its length if too long is not suitable for the incorporation of the oligonucleotide into cells. In consequence, when the oligonucleotide or a derivative thereof of the present invention is used for the control of the expression of Fas ligand by incorporating it into cells, it is preferable that said oligonucleotide or a derivative thereof contains a sequence which is complementary to the Fas ligand gene or mRNA for the Fas ligand and comprises 15 to 30 bases, preferably 15 to 25 bases, more preferably 18 to 22 bases.

With the advance in the antisense techniques, various oligonucleotide derivatives have been found with the aim of improving effects of oligonucleotides as pharmaceutical preparations, such as those having improved affinity for DNA or mRNA of interest, as well as those having improved tissue selectivity, cell permeability, nuclease resistance and intracellular stability.

10

As described in the foregoing, the "oligonucleotide derivative" of the present invention includes all kinds of derivatives including those which contains a base, a sugar, a phosphoric acid moiety and a backbone structure which do not exist in nature.

Examples of generally known derivatives include those in which entire portion or a part of the backbone structure has phosphodiester bonding, phosphorothicate bonding, phosphotriester bonding, methylphosphonate bonding, phosphoramidate bonding, phosphorodithicate bonding or morpholino group [Y. Shoji, *Gan to Kagaku Ryoho* (Cancer and Chemotherapy), vol. 20, pp. 1899 - 1907, 1993]. Also included are polyamide-nucleic acid (PAN) (P.E. Nielsen et al., Science, vol. 2 54, pp. 1497 - 1500, 1991) and certain derivatives in which the 2'-position of the sugar is substituted with other atom or substituent (α-ribose and the like) (Michael J. Gait, pp. 290 - 299; in *Antisense Research and Applications*, CRC Press Inc, Florida, 1993).

Also known as oligonucleotide derivatives are those in which the sugar moiety is substituted with other substance, certain bases are substituted with inosine (called universal base because of its ability to bind to A, T, C and G) and cholesterol, acridine, poly-L-lysine, psoralen, long alkyl chain or the like is linked to the 5'- or 3'-end or inside of an oligonucleotide (Makoto Matsukura, pp. 506 - 519, Paul S. Miller *et al.*, pp. 190 - 202; in *Antisense Research and Applications*, CRC Press Inc, Florida, 1993).

The oligonucleotide derivative of the present invention include all derivatives including these derivatives exemplified above. However, said oligonucleotide derivative may preferably be a derivative in which at least one of its nuclease resistance, tissue selectivity, cell permeability and affinity is improved.

Particularly preferably, said oligonucleotide derivative is a derivative which has phosphorothicate bonding as its backbone structure.

The following describes a process for the production of the oligonucleotide and its derivatives of the present invention.

Oligonucleotides and their derivatives can be produced by known methods (see for instance, *Antisense Research and Applications*, ed. by Stanley T. Crooke and Bernald Lebieu, CRC Press Inc, Florida, 1993).

In the case of natural DNA or RNA, the oligonucleotide of the present invention can be obtained by chemically synthesizer or carrying out PCR using the Fas ligand gene as a template. Also, certain oligonucleotide derivatives such as of methylphosphonate type, phosphorothioate type and the like can be synthesized making use of a chemical synthesizer (for example, Model 394 Perkin-Elmer Japan). In that case, an oligonucleotide of interest or its derivative can be obtained also by carrying out operation of the chemical synthesizer in accordance with the manual attached thereto and purifying the thus synthesized product by an HPLC aided with a reverse chromatography or the like.

Next, use of the oligonucleotide and a derivative thereof of the present invention is described.

When the oligonucleotide and a derivative thereof of the present invention are used as diagnostic probes, they are labeled with a radioisotope, an enzyme, a fluorescent material, a luminescent material or the like in accordance with a usually used method. Next, DNA or mRNA is prepared from cells of a patient to be examined for the expression of Fas ligand, the thus prepared DNA or mRNA as a sample to be tested is allowed to react with the labeled probe prepared above and then the reaction mixture is washed to remove unreacted labeled probe. When the Fas ligand gene or RNA is present in the sample to be tested, said oligonucleotide or a derivative thereof binds to the gene or RNA. The presence of the thus bound product can be detected by using the labeled enzyme, fluorescent material, luminescent material or radioisotope as a marker.

Since relationship between expression of Fas ligand and autoimmune diseases and related information have been reported in recent years, diagnostic probes prepared by the use of the oligonucleotide of the present invention can be used for the diagnosis of autoimmune diseases such as rheumatism, SLE and the

like. In addition, since the Fas ligand is also considered to be related to the cytotoxicity caused by T cells at the time of inflammation, such probes can also be used in diagnosis for the determination of the degree of inflammation and the therapeutic method.

When the oligonucleotide and a derivative thereof of the present invention is used for pharmaceutical purposes, it is desirable to use them with a purity which is suitable for use in pharmaceutical preparations and by pharmacologically acceptable use method.

The oligonucleotide or a derivative thereof of the tenth aspect of the present invention may be used by dissolving or suspending it directly in an appropriate solvent, or by enclosing it in liposomes or integrating it in an appropriate vector. As occasion demands, the oligonucleotide or a derivative thereof of the present invention may be used in appropriate dosage forms such as injections, tablets, capsules, eye drops, creams, suppositories, sprays, cataplasmas and the like, by mixing it with pharmacologically acceptable additive agents such as solvents, bases, stabilizing agents, antiseptics, solubilizing agents, fillers, buffers and the like.

The oligonucleotide or a derivative thereof of the present invention can be used by setting its administration method and dose depending on the age and sex of each patient and the kind and degree of each disease. In other words, it may be used in a dose which is effective in controlling apoptosis and hence in improving morbid states, by selecting a proper route of administration from oral administration and parenteral administration such as inhalation, percutaneous absorption, ophthalmic administration, vaginal administration, intraarticular injection, rectal administration, intravenous injection, topical application, intramuscular injection, subcutaneous injection, intraperitoneal administration and the like.

Finally, a screening method as a eleventh aspect of the present invention is described.

The screening method of the eleventh aspect of the present invention is characterized by the use of a novel polypeptide of the first and the second aspects of the present invention or a transformant transformed in such a manner that it expresses the polypeptides.

According to the screening method of the eleventh aspect of the present invention, substances which bind to the Fas ligand and other substances which exert influences upon expression of the Fas ligand can be screened. All substances including compounds, peptides, proteins, antibodies, nucleic acids and the like are included in the substances to be screened.

In addition, diagnosis of Fas ligand-related diseases can be made making use of the screening method of the present invention.

For example, the presence of abnormality in the function or expression of Fas antigen in a patient of an autoimmune disease can be diagnosed by isolating blood cells or tissue cells from the patient, allowing the isolated cells to react with the Fas ligand or the transformant which expresses the Fas ligand and then observing degree of apoptosis generated in the cells isolated from the patient. With reference to the result of the diagnosis, means for the treatment of the disease can be selected corresponding to its cause.

In addition to the Fas ligand or Fas ligand-expressing transformant, it is preferable to use Fas antigen-expressing cells in the screening method of the present invention. By the use of such a method, not only substances which bind to the Fas ligand or enhance or inhibit expression of the Fas ligand but also other substances which exert influences upon the function of the Fas ligand on cells, substances which enhance or inhibit expression of the Fas antigen and the like, can be screened. Though typical example of the function of the Fas ligand on cells is the induction of apoptosis, said screening method can be used suitably for the screening of not only substances which enhance or inhibit apoptosis but also other substances which enhance or inhibit certain changes generated in Fas antigen-expressing cells in the presence of the Fas ligand.

The screening method of the presnet invention may include any steps. However, preferably, the screening method of the present invention includes a step selected from the following steps (1) to (3);

(1)

45

50

55

- (a) one selected from the group consisting of a Fas ligand, a Fas ligand-expressing transformant and culture supernatant of the transformant is cultured together with cells which express Fas antigen,
- (b) a substance to be tested or a sample containing the substance to be tested is added to the above system (a), and
- (c) at least 1 item selected from viability, morphological changes and biochemical changes in the Fas antigen-expressing cells is measured,

(2)

- (a) a substance to be tested or a sample containing the substance to be tested is incubated together with one selected from the group consisting of a Fas ligand, a transformant which expresses the Fas ligand and culture supernatant of the transformants,
- (b) cells which express Fas antigen are added to the above system (a), and cultured, and

(c) at least 1 item selected from viability, morphological changes and biochemical changes in the Fas antigen-expressing cells is measured, and

5

10

- (a) a substance to be tested or a sample containing the substance to be tested is incubated together with cells which express Fas antigen,
- (b) a Fas ligand, a transformant which expresses the Fas ligand or culture supernatant thereof is added to the above system (a) and cultured, and
- (c) at least 1 item selected from viability, morphological changes and biochemical changes in the Fas antigen-expressing cells is measured.

Method for the measurement of the viability, morphological changes or biochemical changes in the Fas antigen-expressing cells is not particularly limited, provided that it can detect such changes. The presence and degree of apoptosis in Fas antigen-expressing cells can be measured based on the amount of released ⁵¹Cr incorporated in advance in the Fas antigen-expressing cells. The number of survived cells, namely, number of not-apoptotic cells of the Fas antigen-expressing cells may be measured by trypan blue staining or an assay in which formation of formazan is used as a marker (MTT assay, Almarl Blue assay or the like).

The screening method of the present invention, is preferably characterized by the use of the polypeptide represented by any one of the formulae 1 to 12, or the transformant expressing thereof.

It is generally conceived that a membrane protein present at the cell surface binds to other molecules by its extracellular domain. Accordingly, in the screening method according to the eleventh aspect of the invention, it would be preferable to use the polypeptides having the amino acid sequence of formulae 1 to 3, 5 to 7, and 9 to 11, and the transformants capable of expressing such polypeptides. And in particular, the polypeptides having the amino acid sequence of formulae 1 to 3, and the transformants capable of expressing thereof are preferable. The polypeptide used in the screening may be produced by the process described for the seventh aspect of the present invention, and the transformant capable of expressing the polypeptide may be produced by the process described for the fifth or sixth aspect of the present invention.

According to the screening method of the eleventh aspect of the present invention, substances which bind to the Fas ligand and other substances which exert influences upon expression of the Fas ligand can be screened.

The term "substance" as used herein is not limited to any particles substance, and may be designate a compound, a peptide, a protein, an antibody, a nucleic acid, or the like. The screening as described above may be also be utilized in the diagnosis of the Fas ligand-associated diseases.

For example, the presence/absence of abnormality in the function of the Fas antigen of a patient suffering from an autoimmune disease can be diagnosed by isolating blood cells or cells of tissue origin from the patient, and reacting the thus isolated cells with the Fas ligand or the transformant capable of expressing the Fas ligand to observe the degree of apoptosis induced in the cells isolated from the patient. A suitable treatment may then be selected by taking the results of such diagnosis into consideration.

Any type of cells may be used as the Fas antigen-expressing cells, such as cells in which expression of the Fas antigen is induced by a virus or a drug like the case of AIDS virus-infected cells, or an established cells, a hybridoma or a transformant which expresses the Fas antigen. It is preferable to use human Fas antigen-expressing cells, especially cells of a human Fas antigen-expressing transformant such as WC8 cells (Itoh N. et al., J. Immunol., vol. 151, pp. 621 - 627, 1993).

EXAMPLES

The following examples are provided to further illustrate the present invention. It is to be understood, however, that the examples are for purpose of illustration only and are not intended as a definition of the limits of the present invention.

The abbreviations used in the following descriptions are based on those which are commonly used in the related technical field.

Basic procedures described in the following examples were carried out in the light of "Molecular Cloning, A Laboratory Manual", 2nd ed. (Sambrook J. et al., Cold Spring Harbor Laboratory, 1989), "Introduction of Recombinant Genes into Cells and Expression of the Genes" (Imamoto F. et al., Protein, Nucleic Acid and Enzyme, supplement 28 (14), 1983; written in Japanese) and "General Cell Technological Techniques" (Okada Y., Experimental Medicine, supplement 7 (13), 1989; written in Japanese).

(Inventive Example 1) Preparation of chimera protein

(1) Preparation of expression plasmid pFas-FcII

A plasmid, pFas-FcII, for use in the expression of a chimera protein (to be referred to as "mFas-Fc" hereinafter) of the extracellular domain of mouse Fas (mFas) antigen and the Fc region of human IgG1 (hIgG1) was prepared in the following manner to be used in Inventive Example 2.

Firstly, oligonucleotide primers containing a sense sequence in intron 4 (GATTTTCAACCACTCAGTCG) SEQ ID NO: 33 and an antisense sequence in intron 5 (ATGCGGCCGCTGGATCCTTTGTATGAAATTGAGTAAT) SEQ ID NO: 34 of the mouse Fas antigen chromosomal gene were synthesized chemically. The latter oligonucleotide primer contained a *BamH*I site. Using these oligonucleotide primers, PCR was carried out making use of a plasmid containing mouse Fas antigen chromosomal gene (pMF3ES; annual meeting of the Society of Molecular Biology, 1992) as a template. As the result, a DNA fragment of 383 bp having flanking regions at the 5'- and 3'-ends of the exon 5 was amplified.

The thus amplified product was digested with *Pst*I and *Bam*HI to obtain a DNA fragment of 128 bp containing the 3'-end of the exon 5 and a part of the intron 5. With the thus obtained DNA fragment, a *PstI-Bam*HI DNA fragment moiety of a plasmid pMF1 (Watanabe-Fukunaga R. *et al.*, *J. Immunol.*, vol. 148, pp. 1274 - 1279, 1992) was replaced to prepare a plasmid pMFX.

Separately from this, a plasmid pMH4 which contains an exon for the human lgG1 heavy chain constant region (Nishimura Y. et al., Cancer Res., vol. 47, pp. 999 - 1005, 1987) was digested with Haell, and the resulting DNA fragment of 1.7 kbp was subcloned into the Xbal site of pBluescript KS(+).

This was digested with *Hinc*II and *Apa*I to obtain a DNA fragment of 1.4 kbp containing exons coding for hinge, CH2 and CH3 domains. This fragment was inserted into the *Xba*I site of the aforementioned plasmid pMFX to prepare a plasmid pFas-Fc. The plasmid pFas-Fc was digested with *Kpn*I, blunt-ended and then digested with *Not*I. Thereafter, the thus obtained DNA fragment of 2.3 kbp was ligated to a mammalian expression vector pEF-BOS (Mizushima S. and Nagata S., *Nucleic Acids Res.*, vol. 18, p. 5332, 1990) to obtain the expression plasmid pFas-FcII of interest.

(2) Preparation of expression plasmid phTNFR_{\$\beta\$}-Fc

30

50

A plasmid phTNFR β -Fc for use in the expression of a chimera protein (to be referred to as "hTNFR β -Fc" hereinafter) of TNF receptor β and Fc region of human lgG1 was constructed in the following manner to be used in Inventive Example 2.

Firstly, a plasmid p55TNFr-HG1 (Leostscher H. et al., J. Biol. Chem., vol. 266, pp. 18324 - 18329, 1991) was digested with *KpnI* and *HindIII* to prepare a DNA fragment of 650 bp. The plasmid p55TNFr-HG1 is a plasmid containing a cDNA sequence which encodes the extracellular domain of human TNF receptor (p55) contiguous to an artificial splice donor sequence.

Separately from this, the plasmid pFas-FcII was digested with *Hin*cII and *Hin*dIII. Thereafter, a DNA fragment of about 700 bp containing a sequence coding for the extracellular domain of mouse Fas antigen was exchanged with the aforementioned 650 bp *Kpn*I-*Hin*dIII fragment to obtain the plasmid phTNFR\$\beta\$-Fc of interest.

(3) Preparation of expression plasmid pBF-Fc1

A plasmid pBF-Fc1 for use in the expression of a chimera protein (to be referred to as "hFas-Fc" hereinafter) of the human Fas antigen extracellular domain and Fc region of human IgG1 was constructed in the following manner to be used in Inventive Example 10.

Firstly, a plasmid pBLF58-1 containing a human Fas antigen-encoding DNA fragment (Itoh N. *et al.*, *Cell*, vol. 66, pp. 233 - 243, 1991) was digested with *Xho*I and *Bam*HI to obtain a fragment of 700 bp. Next, the plasmid pFas-Fc used in the construction of the chimera protein mFas-Fc expression vector was digested with *Xho*I and *Bam*HI, and the 700 bp fragment obtained above was inserted into the digested product to obtain an expression plasmid pBHF-C1.

Separately from this, a fragment in which an intron 5 sequence of the mouse Fas antigen chromosomal gene and a *BamH*I site is added to a sequence coding for the extracellular domain of human Fas antigen was prepared by carrying out PCR using a sense primer 1 (ATGCCCAAGTGACATCAACT) SEQ ID NO: 35 and an antisense primer 1 (GCGCGGATCCAGGAAGTGGGAAAGGATTACCTTCCTCTTTGCACTTGGTG) SEQ ID NO: 36 making use of pBLF58-1 as a template.

The thus obtained PCR product was digested with *Mscl* and *BamHI*, and the resulting DNA fragment of 360 bp was inserted into pBHF-C1 which has been digested in advance with *Mscl* and *BamHI*. Next, the thus obtained plasmid was digested with *KpnI*, blunt-ended and then digested with *Not*I to obtain a DNA fragment coding for the extracellular domain of human Fas antigen and Fc region of human lgG1. Thereafter, the thus obtained fragment was inserted into pEF-BOS which has been digested with *BstXI*, blunt-ended and then digested with *Not*I, thereby obtaining the human Fas-Fc expression vector pBF-Fc1.

(4) Production and purification of chimera protein

10

20

35

COS-7 cells and BTS-1 cells (Sedivy J.M., *Biol. Technology*, vol. 6, pp. 1192 - 1196, 1993) were respectively transfected with plasmids pFas-FcII and phTNFR_B-Fc. COS-7 cells were also transformed with plasmid pBF-Fc1.

Transfection of COS-7 cells was carried out in accordance with the DEAE-dextran method reported by Fukunaga R. et al. (Cell, vol. 61, pp. 341 - 350, 1990). After completion of the transformation, transformed COS-7 cells were incubated for 24 hours in a medium containing 10% of FCS (fetal calf serum) and then for 48 hours and 72 hours in a serum-free medium. Thereafter, the resulting culture supernatants were collected, centrifuged, filtered through a 0.45 μ m filter to remove cell debris and then subjected to a column chromatography using protein A-Sepharose 4B (Pharmacia) to purify chimera proteins mFas-Fc, hTNFR β -Fc and hFas-Fc, respectively.

On the other hand, transfection of BTS-1 cells was carried out by means of electroporation (Potter H. *et al., Proc. Natl. Acad. Sci. USA*, vol. 81, pp. 7161 - 7165, 1984). That is, after digesting plasmid pFas-FcII with *Apa*LI, and plasmid phTNFR\$-Fc with *Sac*I, 1 x 10⁷ of the cells were transformed with 50 µg of each of the resulting plasmid DNA fragments together with 5 µg of *Xho*I-digested pSTneoB. After 10 days of selection using D-MEM containing 10% FCS and 300 µg/mI of G-418, G-418 resistant clones were isolated and cultured at 39.5 °C.

In order to identify a clone which produces the chimera protein of interest, some of the isolated clones were cultured at 33°C for 3 days, and the chimera protein secreted into the medium was inspected by enzyme-linked immunosorbent assay (ELISA). In the ELISA, anti-human IgG-Fc antibody (Cappel, 55071) was used as the capture antibody and horseradish peroxidase-labeled anti-human IgG-Fc antibody (Jackson Immunoresearch Lab, 109-035098) was used as the detection antibody.

Each of two transformants capable of producing mFas-Fc and hTNFR\$-Fc respectively in high efficiency was cultured at 39.5 °C and then inoculated into a 15 cm plate to 50% confluent. After 1 week of culturing at 33 °C, mFas-Fc and hTNFR\$-Fc were purified respectively from the resulting culture supernatants by protein A-Sepharose 4B column (Pharmacia) chromatography.

When the thus purified mFas-Fc was analyzed by SDS-PAGE, a band was observed at a position corresponding to a molecular weight of 55 kD under a reducing condition, and under a non reducing condition a band was observed at a position corresponding to a molecular weight of 110 kD. These results indicate that the thus obtained chimera protein mFas-Fc exists as a homodimer formed by S-S bonding.

(Inventive Example 2) Analysis by flow cytometry and selection of d10S-2 cell line

(1) Biotinylation and FITC labeling of chimera protein

Biotinylation of mFas-Fc and hTNFRβ-Fc was carried out using sulfosuccinimidyl 6-(biotinamide) hexanoate (NHS-LC-biotin, Pierce Chemical, 21335) in accordance with the manufacturer's instructions.

Separately from this, 1 mg of hTNFR\$-Fc and 20 µg of fluorescein isothiocyanate (FITC) were mixed in 1 ml of 50 mM sodium carbonate buffer (pH 9.5) and allowed to react with each other at room temperature for 4 hours. Thereafter, unbound FITC was removed by a column chromatography making use of Sephadex G-25M to obtain FITC-labeled hTNFR\$-Fc.

(2) Flow cytometry

PC60-d10S cells (to be referred to as "d10S" hereinafter; Rouvier E. et al., J. Exp. Med., vol. 177, pp. 195 - 200, 1993) were washed with a staining solution (phosphate-buffered saline (to be referred to as "PBS" hereinafter) containing 2% FCS and 0.02% NaN₃). About 1 x 10⁶ of the cells were suspended in 50 μl of the staining solution supplemented with 5 μg/ml of rat anti-mouse Fc_γRll blocking antibody (Pharmingen). This suspension was dispensed into wells of a 96 well plate and incubated for 10 minutes on an ice bath. A 20 μg/ml solution of the biotinylated mFas-Fc was dispensed into wells of the resulting plate

in 50 µl portions, and the incubation was continued for additional 30 minutes on an ice bath. After washing the plate with the staining solution, phycoerythrin-labeled streptoavidin (25 times dilution, Becton Dickinson) was added to each well, the contents in each well was adjusted to 100 µl with the staining solution and then the reaction was carried out for 30 minutes on an ice bath.

After washing the cells with the staining solution, cytometric analysis was carried out using FACScan (Becton Dickinson). As the result, a slight shift in the fluorescence intensity was observed which confirmed that said cells were stained with the biotinylated mFas-Fc (see Fig. 1a). Control was expressed as an open area, and staining before 4 hours of treatment with PMA and ionomycin as a stippled area and staining after 4 hours of treatment with PMA and ionomycin as a closed area.

Contrary to this, staining was not observed when the d10S cells treated in the same manner with the biotinylated hTNFR\$-Fc were analyzed by the flow cytometry. On the basis of these results, it was confirmed that the mFas-Fc prepared in Inventive Example 1 binds to the Fas ligand on the d10S cells in specific fashion.

15 (3) Screening of d10S-2 cell strain

A total of $1\text{-}3 \times 10^7$ of the d10S cells which showed a high fluorescence activity in the above step (2) were allowed to react with the biotinylated mFas-Fc and FITC-labeled hTNFR β -Fc in the same manner as described above, stained with phycoerythrin-labeled streptoavidin and then subjected to cell sorting using FACScan (Becton Dickinson). Cells which emitted the phycoerythrin fluorescence at high levels (upper 0.3 to 0.5% of the cells) were collected and cultured using D-MEM (Dulbecco's modified Eagle's Medium) containing 10% FCS and 50 nM 2-mercaptoethanol.

The cells thus sorted out were subjected to the above sorting procedure repeatedly, and the finally selected cell group was named d10S-2. The d10S-2 cell strain is a group of highly concentrated cells capable of showing a high Fas ligand expression quantity both in the presence and absence of stimulating agents (see Fig. 1b).

(Inventive Example 3) Construction of cDNA library

The d10S-2 cells obtained in Inventive Example 2 were cultured in D-MEM containing 10% FCS until the cell density reached 2 x 10⁵ cells/ml and then stimulated with 20 ng/ml of PMA and 1 μg/ml of ionomycin at 37 °C for 3 hours. After isolating total RNA by the guanidine isothiocyanate/acid phenol method (Chomczynski P. and Sacchi N., *Anal. Biochem.*, vol. 162, pp. 156 - 159, 1987), poly (A) RNA was selectively isolated by repeating an oligo(dT)-cellulose column chromatography twice. Using a random hexamer or an oligo(dT) primer, double-stranded cDNA was synthesized in accordance with the procedure of Itoh N. *et al.* (*Cell*, vol.66, pp. 233 - 243, 1991). After adding a *Bst*Xl adapter to the thus obtained double-stranded cDNA, molecular weight fractionation was carried out by 1% agarose gel electrophoresis. Molecules of cDNA having a size of 1.5 kbp or more were recovered and ligated to a pCEV4 vector (Itoh N. *et al.*, *Cell*, vol. 66, pp. 233 - 243, 1991) which has been digested with *Bst*Xl in advance. Using the ligation product, *E. coli* DH10B cells (Gibco BRL) were transformed by means of electroporation (Dower W. *et al.*, *Nucleic Acids Res.*, vol. 16, pp. 6127 - 6145, 1988). About 1.0 x 10⁶ independent clones obtained from the oligo(dT)-primed cDNA library were mixed with about 1.3 x 10⁶ clones obtained from the random hexamer-primed cDNA library to prepare plasmid DNA for use in the transformation of COS-7 cells.

(Inventive Example 4) Concentration of cDNA clone by panning

Transformation of COS-7 cells with the plasmid DNA obtained in Inventive Example 3 was carried out by electroporation. That is, 5×10^6 of the COS-7 cells were washed with K-PBS⁻ (a buffer solution containing 30.8 mM NaCl, 120.7 mM KCl, 8.1 mM Na₂HPO₄ and 1.46 mM KH₂PO₄) and suspended in 0.4 ml of K-PBS supplemented with 5 mM MgCl₂ (K-PBS⁺).

Next, 40 µg of the plasmid DNA was dissolved in 0.4 ml of K-PBS+ and added to the above cell suspension, and the mixture was incubated for 10 minutes on an ice bath. Electroporation was effected by applying 230 V of voltage to the cells with a capacitance of 960 µF. After 10 to 15 minutes of incubation on an ice bath, the cell suspension was diluted with 5 ml of cold serum-free D-MEM and incubated for 30 minutes at room temperature. Thereafter, the thus treated cells were inoculated into two plates having a diameter of 10 cm and cultured at 37 °C for 60 hours in D-MEM containing 10% FCS.

In the above procedure, a total of 1.2 x 10⁸ COS-7 cells were transformed and cultured in the 10 cm plates. A 5 ml portion of PBS/EDTA/NaN₃ (PBS supplemented with 0.5 mM EDTA and 0.02% NaN₃) was

added to each of the resulting plates and incubated at 37° C for 30 minutes. The thus treated cells were detached from the plate and suspended again in PBS/EDTA/NaN₃ containing 3 mg/ml of BSA and 2.5 μ g/ml of anti-mouse Fc γ II receptor antibody, with a cell density of 5-7 x 10^6 cells/ml. After 10 minutes of incubation on an ice bath, mFas-Fc was added to a final concentration of 4 μ g/ml and the resulting cell suspension was incubated again for 60 minutes on an ice bath. The thus treated cells were washed with ice-cold PBS and suspended to a cell density of 5-7 x 10^6 cells/ml in PBS supplemented with 50 mM HEPES buffer (pH 8.3) and 0.2 mM bis(sulfosuccinimidoyl) suberate (BS³, Pierce Chemical). After 30 minutes of incubation on an ice bath, 1 M Tris-HCl buffer (pH 8.0) was added to a final concentration of 50 mM, and the resulting cell suspension was incubated for 10 minutes on an ice bath. The thus treated cells were washed with PBS and suspended in 30 ml of PBS/EDTA/NaN₃ which has been supplemented with 3 mg/ml of BSA, and the suspension was filtered through a nylon mesh of 100 μ m in pore size to remove aggregated materials.

The cell suspension was dispensed into 30 panning plates (10 cm in diameter) to which anti-human IgG-Fc antibody (Cappel, 55071) has been immobilized in advance. After 2 hours of incubation at room temperature, non-adherent cells were removed by gentle washing with PBS, and extrachromosomal DNA was extracted from the adherent cells in accordance with the procedure of Itoh N. et al. (Cell, vol. 66, pp. 233 - 243, 1990). Using the thus obtained DNA by the first panning, transformation of E. coli cells was carried out by means of electroporation to obtain 4.1 x 10⁶ colonies. Using plasmid DNA prepared from these colonies, 9.6 x 10⁷ COS-7 cells (60 plates) were transformed.

Second panning was carried out by dispensing the thus transformed cells into 30 panning plates, and plasmid DNA was prepared from the adherent cells in the same manner as the first panning. Using the thus recovered plasmid DNA, transformation of E. coli cells were carried out to obtain 8.0×10^6 clones. Using plasmid DNA prepared from these colonies, 4.0×10^7 COS-7 cells (10 plates) were transformed.

Third panning was carried out by dispensing the thus transformed cells into 30 panning plates. Plasmid DNA was prepared from the adherent cells in the same manner as the first and second pannings and used for the transformation of E. coli cells to obtain 3.8 x 10^6 clones. Using plasmid DNA prepared from these colonies, 1.0×10^7 COS-7 cells (25 plates) were transformed and dispensed into 10 panning plates to carry out fourth panning.

After completion of the fourth panning, extrachromosomal DNA was prepared from COS-7 cells and used for the transformation of *E. coli* cells. When plasmid DNA was prepared from each cell clone and analyzed, 16 of 48 clones contained plasmid DNA molecules each having an insert of 1.0 kbp or more. Each of these plasmid DNA molecules was introduced into COS-7 cells which were subsequently subjected to staining with the biotinated mFas-Fc and then to flow cytometry in accordance with the method of Inventive Example 2. As the results, 5 clones were found to be stained. Fig. 1c shows a result of the flow cytometry of COS-7 cells (COS/pTN24-15) transfected with one of these 5 clones, pTN24-15, which contains an insert of 1.6 kbp. The COS-7 cells transfected with pTN24-15 were not stained with the biotinylated hTNFRβ-Fc. Also, COS-7 cells transfected with pCEV4 having no foreign gene were not stained with the biotinylated mFas-Fc.

40 (Inventive Example 5) Determination and analysis of DNA sequence

20

When the 5 clones obtained in Inventive Example 4 were analyzed by restriction enzyme mapping, it was found that they were overlapped with one another. In consequence, pTN24-15 as one of these 5 clones was further analyzed in detail. Determination of DNA sequence was carried out making use of a DNA sequencer (Model 370A, Perkin-Elmer Japan) and Taq Dye Deoxy Cycle Sequencing Kit (Perkin-Elmer Japan).

Nucleotide sequence of the clone pTN24-15 and an amino acid sequence deduced from the nucleotide sequence are shown in Figs. 2 and 3 and SEQ ID NO: 25. This cDNA is composed of 1,623 bases and contains one open reading frame.

Though the sequence "CCA/GCCATGG" (SEQ ID NO: 37) proposed by Kozak M. (*J. Cell Biol.*, vol. 115, pp. 887 - 903, 1991) was not found in this sequence, its translation initiation site was considered to be ATG of the positions 74 to 76. The open reading frame is terminated with the termination codon TAA of the positions 908 to 910. It was found also that this cDNA encodes 278 amino acid residues. The molecular weight deduced from the amino acid sequence is 31,138, with an isoelectric point of 9.53.

Among 278 amino acid residues encoded by the cDNA, a sequence of 77 amino acid residues of the N-terminal side was found to be extremely rich in proline. Though a typical signal sequence was not found in the area of the N-terminal side, a hydropathy analysis confirmed the presence of 22 hydrophobic amino acid residues contiguous to the proline-rich region, which seemed to have a function as a transmembrane

anchor. Because of the absence of signal sequence and the presence of inner hydrophobic domain, it was suggested that the Fas ligand is a type II transmembrane protein.

It was confirmed that an assumed region as the extracellular domain is present in the C-terminal side, which is composed of 179 amino acid residues and contains four N-glycosylation sites (Asn-X-Ser/Thr). These glycosylation sites are shown by "in Figs. 2 and 3.

The d10S-2 cell strain used in the construction of cDNA library is a hybridoma of rat and mouse cells. In order to determine origin of the Fas ligand cDNA, primers were designed from the 3'-end noncoding region of the Fas ligand cDNA and synthesized to carry out PCR in which chromosomal DNA preparations obtained from rat and mouse splenocytes are used as templates respectively. That is, in the sequence of SEQ ID NO: 25, nucleotide positions 1006 to 1025 and 1305 to 1324 were used as sense primers 2 and 3 (SEQ ID NOS: 38 and 39), and positions 1327 to 1346 and 1543 to 1562 as antisense primers 2 and 3 (SEQ ID NOS: 40 and 41). As the results, bands of 341 bp and 258 bp in size were obtained only with the rat chromosomal DNA. These results suggest that the cDNA obtained from the clone pTN24-15 is originated from the rat gene in the d10S-2 hybridoma cells.

In this connection, *E. coli* cells were transformed with the aforementioned pTN24-15 in accordance with the method of Hanahan D. *et al.* ("Techniques for Transformation of *E. coli*", in *DNA Cloning*, vol. 1, ed. by Glover D.M., pp. 109 - 136, IRL Press, 1985). A resulting transformant, named DH10B(pTN24-15), has been deposited in National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology, and has been assigned the designation as FERM P-13953, which was subsequently transferred to the International Depository Authority on October 27, 1994, as FERM BP-4848.

(Inventive Example 6) Northern hybridization

15

Using a mRNA isolation kit (Pharmacia), poly (A) RNA was prepared from d10S, d10S-2, rat tissues (the brain, lungs, heart, liver, small intestines, kidney, ovaries, testes skeletal muscle) and rat cells (splenocytes and thymocytes). The RNA was denatured by heating at 65°C for 5 minutes in 50% formamide, subjected to electrophoresis using 1.5% agarose gel containing 6.6% formaldehyde and then transferred on a nitrocellulose or nylon membrane (Schleicher and Schuell).

As a probe, a double-stranded DNA fragment of 925 bp containing a DNA sequence SEQ ID NO: 42 comprising the positions 43 to 967 of the pTN24-15 obtained in Inventive Example 4 was prepared by PCR and ³²P-labeled making use of a random primer labeling kit (Boehringer-Mannheim). A 1.8 kbp *Bam*HI fragment of human EF1α cDNA (Uetsuki T. *et al., J. Biol. Chem.*, vol. 264, pp. 5791 - 5798, 1989) was labeled with ³²P and used as a control probe. The hybridization was carried out under high stringency condition in accordance with the method of Sambrook J. *et al.* (*Molecular Cloning, A Laboratory Manual*, 2nd ed., Cold Spring Harbor Laboratory, New York, 1989).

Fig. 4 shows results of the northern hybridization in which d10S, d10S-2 and d10S-16 cells were respectively stimulated or not stimulated with PMA and ionomycin. As is evident from Fig. 4, the poly (A) RNA obtained from d10S cells showed a weak hybridization band of about 2.0 kbp. Strength of the signal of this band increases when d10S cells are stimulated with PMA and ionomycin. The poly (A) RNA obtained from d10S-2 cells showed a signal which was about 4 times stronger than that from d10S cells stimulated with PMA and ionomycin, indicating that the expression quantity of Fas ligand mRNA in d10S-2 cells is about 4 times higher than that in d10S cells.

In the case of the d10S-16 cells which has been obtained after 16 repetitions of the procedure of Inventive Example 2, the expression quantity of mRNA was about 100 times higher than the case of d10S cells. Since the cytotoxic activity of d10S-16 cells was 100 times higher than that of d10S cells, it was found that increase in the expression quantity of the Fas ligand mRNA has positive correlations with the cytotoxic activity and the staining strength by mFas-Fc.

Fig. 5 shows results of the northern hybridization of splenocytes and thymocytes prepared from the spleen and the thymus of rat, comparing just after their preparation (before culturing), after their culturing at 37 °C for 8 hours without stimulating agent (untreated) and after their culturing at 37 °C for 8 hours in the presence of each stimulating agent. In the rat splenocytes, weak expression of the Fas ligand mRNA was observed. When the rat splenocytes were stimulated for 8 hours with PMA and ionomycin or ConA and IL-2, amount of the Fas ligand mRNA increased markedly. In the case of rat thymocytes, expression of the Fas ligand mRNA was hardly found before their culturing and after their untreated culturing. However, when the rat thymocytes were stimulated with PMA and ionomycin or ConA and IL-2, expression level of the Fas ligand mRNA increased to the same level of the case of splenocytes (Fig. 5).

When expression level of the Fas ligand mRNA in each rat tissue was examined, a band of about 2.0 kbp having a strong signal was found in testis (Fig. 6). Bands having normal or weak signals were found in

the small intestine, kidney and lung, but expression of the Fas ligand mRNA was not found in other tissues.

In this instance, all mRNA molecules were evidently intact, because a band of 1.8 kbp was found in all cells and tissues rehybridized with the human EF1α cDNA probe (the lower column in each of Figs. 4, 5 and 6).

(Inventive Example 7) Biochemical analysis of Fas ligand

The Fas ligand expressed in d10S-12 cells and the Fas ligand expressed in COS-7 cells which have been transfected with pTN24-15 were checked for their biochemical properties.

The d10S-16 cells are a cell population which has been obtained after 12 repetitions of the procedure of Inventive Example 2. Firstly, the cell surface protein of the d10S-12 cells or the COS-7 cells transfected with pTN24-15 was biotinated by the method of Meier et al. (Anal. Biochem., vol. 204, pp. 220 - 226, 1992) in which D-biotinyl-ε-aminocaproic acid N-hydroxysuccinimide ester (biotin-CNHS-ester, Boehringer Mannheim) is used. In this case, COS-7 cells transfected with the pCEV4 vector which does not contain extrinsic gene were used as a control of the COS-7 cells transfected with pTN24-15. Cells (7.5 x 10⁶) were added to 1 ml of a lysis buffer (1% NP-40, 50 mM Tris-HCl (pH 8.0), 150 mM NaCl, 1 mM (p-aminophenyl)-methylsulfonyl fluoride hydrochloride (APMSF), 1 μg/ml pepstatin and 1 mM leupeptin) and incubated for 30 minutes on an ice bath to effect cell lysis.

After 15 minutes of centrifugation at 14,000 rpm, the resulting supernatant fluid was incubated with 10 µg/ml of hTNFRβ-Fc for 60 minutes on an ice bath and then with a 5% volume of protein A-Sepharose 4B for 60 minutes at 4 °C. After removing protein A-Sepharose 4B, 10 µg/ml of mFas-Fc was added to the resulting supernatant fluid and incubated for 60 minutes on an ice bath. To the resulting mixture was added 1% volume of protein A-Sepharose 4B, followed by overnight incubation at 4 °C. After centrifugation, the precipitate was washed with the lysis buffer, suspended in 20 µl of Laemmli's sample buffer (62.5 mM Tris-HCl buffer (pH 6.3) containing 2% SDS, 10% glycerol and 0.002% Bromophenol Blue) supplemented with 5% 2-mercaptoethanol and then heated at 95 °C for 2 minutes. Thereafter, the thus prepared sample was subjected to a gradient gel electrophoresis using a 10 to 20% gradient polyacrylamide gel containing 0.1% SDS, and the protein molecules were transferred on a PVDF membrane and detected with an ECL system (Amersham).

As shown in Fig. 7, mFas-Fc immunoprecipitated with a protein having a molecular weight of about 40,000 contained in the d10S-12 cell lysate and with a protein having a molecular weight of about 37,000 to 45,000 contained in the lysate of COS-7 cells transfected with pTN24-15 (COS7/pTN24-15). Products of immunoprecipitation were not found in the case of COS-7 cells transfected with the pCEV4 vector which does not contain foreign gene (COS7/pCEV4).

Molecular weight of each of the proteins immunoprecipitated in the COS-7 cells transfected with pTN24-15 and in the d10S-12 cells was larger than the molecular weight deduced from the aforementioned amino acid sequence. The difference in the molecular weight between these two cell populations and the difference between the molecular weight of immunoprecipitated proteins and the molecular weight deduced from the amino acid sequence were considered to be due to different glycosylation occurred in some of the four N-glycosylation sites.

(Inventive Example 8) Measurement of cytotoxicity of Fas ligand

35

Cytotoxic activities of d10S cells and COS-7 cells transfected with pTN24-15 were measured using W4 cells as the target cells (Ogasawara J., et al., Nature, vol. 364, pp. 806 - 809, 1993). The W4 cells are cells which acquired mouse Fas antigen-expressing ability by transformation of mouse WR19L cells that can hardly express mouse Fas antigen and are sensitive to the cytotoxicity of TNF.

Examination of cytotoxic activity was carried out in accordance with the method of Rouvier E. et al. (J. Exp. Med., vol. 177, pp. 195 - 200, 1993).

Firstly, d10S cells (2.5 - 5 x 10⁵ cells/ml) were suspended in 10% FCS-containing D-MEM supplemented with 10 ng/ml of PMA (Sigma Chemical) and 500 ng/ml of a calcium ionophore, ionomycin (Calbiochem). After 3 hours of incubation at 37 °C, the cells were washed with D-MEM to be used as effector cells. Also, COS-7 cells were transfected with pTN24-15 by DEAE-dextran method to be used as effector cells. On the other hand, 1 x 10⁶ of WR19L cells or W4 cells were suspended in 100 µl of RPMI 1640 containing 10% FCS and incubated at 37 °C for 2 hours together with 20 µCi of [5 °Cr] sodium chromate (Amersham). The resulting cells were washed with the culture solution (RPMI 1640) and used as the target cells

1 x 10 4 of 5 Cr-labeled target cells were mixed with effector cells at the various ratios in each well of a round-bottomed microtiter plate. Total volume of the cell suspension in each well was adjusted to 200 μ l. The thus prepared plate was centrifuged at 700 rpm for 2 minutes and then incubated at 37 4 C for 4 hours. After 5 minutes of centrifugation at 1,200 rpm, a 100 μ l portion of supernatant fluid was collected from each well and its radioactivity was measured using a γ counter to calculate specific cytolysis ratio.

Spontaneous release of ⁵¹Cr was determined by incubating the target cells solely in the medium, and maximum release was determined by adding Triton X-100 to the target cells to a final concentration of 0.1%. The specific cytolysis ratio was calculated based on the following formula.

10

15

Specific cytolysis ratio =
$$\frac{A - B}{C - B}$$

- A, experimental release of 51Cr
- B, spontaneous release of 51Cr
- C, maximum release of ⁵¹Cr

As shown in Fig. 9, the COS-7 cells transfected with pTN24-15 (COS/pTN24-15) lysed W4 cells , but lysis of W4 cells was not observed by another COS-7 cells transformed with the pCEV4 vector having no foreign gene (COS/pCEV4). When cytotoxic activities of the COS-7 cells transfected with pTN24-15 (COS/pTN24-15) and d10S cells are compared by their ratio to W4 cells (effector cells/target cells), the former showed at least 10 times higher activity than the latter. In addition, both of the d10S cells and the COS-7 cells transfected with pTN24-15 (COS/pTN24-15) showed no cytotoxicity upon WR19L cells (Figs. 8 and 9).

25

(2) Cytotoxicity by adding of culture supernatant

Fig. 10 shows the examined cytotoxic activity by adding a culture filtrate of various concentrations of the COS/pTN24-15 (the COS-7 cells transfected with pTN24-15) or COS/pCEV4 against the respective effector cells (W4, WR19L).

When cytotoxic activity of a culture supernatant of the COS-7 cells transfected with pTN24-15 (COS/pTN24-15) was examined, significant activity was observed on the W4 cells but not on the WR19L cells (Fig. 10). This result shows that the recombinant Fas ligand was expressed by the COS-7 cells and cleaved to be a soluble form.

35

(3) Inhibition of the cytotoxic activity by mFas-Fc and hTNFRβ-Fc.

In addition, when mFas-Fc and hTNFR\$-Fc were added to the assay system, and the cytotoxicity was examined. The results are shown in Fig. 11. As Fig. 11 shows, the cytotoxicity of the Fas ligand-expressing COS-7 cells (COS/pTN24-15) was inhibited by 10 µg/ml of mFas-Fc but not by the same amount of hTNFR\$-Fc similar to the case of the d10S cells.

(Inventive Example 9) Fragmentation of chromosomal DNA

Using a 24 well plate, 8 x 10⁴ of COS-7 cells in each were transfected with 10 µg of pTN24-15. After 72 hours of the transformation, 2 x 10⁵ of WR19L cells or W4 cells were added to each well and incubated at 37 °C for 1 to 3 hours in RPMI 1640 containing 10% FCS. Non-adherent cells which did not adsorbed to the wall of each well were collected to prepare chromosomal DNA in accordance with the method of Laird P.W. et al. (Nucleic Acids Res., vol. 19, p. 4293, 1991), and the thus prepared DNA was subjected to an agarose gel electrophoresis in the presence of 0.5 µg/ml of ethidium bromide.

The results are shown in Fig. 12. As is evident from the drawing, the chromosomal DNA in the W4 cells co-cultured with COS-7 cells which have been transfected with pTN24-15 (COS/pTN24-15) became fragments in a step-ladder fashion which is an important feature of apoptosis.

The DNA ladder was observed after 1.0 hour of the incubation, and most portion of the DNA became fragments after 2 hours of the incubation.

Such a fragmentation of DNA was not observed in W4 cells co-cultured with COS-7 cells which have been transfected with pCEV4 that contains no foreign gene. In addition, such a fragmentation of DNA was not found in WR19L cells but only in W4 cells co-cultured with transformed COS-7 cells.

(Inventive Example 10) Purification of Fas ligand by affinity chromatography

(1) Biotinylation of cell surface protein

In order to use as a tracer protein in the following experiments, biotinylation of cell surface protein was carried out in accordance with the method of Meier *et al.* (*Anal. Biochem.*, vol. 204, p. 220, 1992). That is, the d10S-12 cells prepared in the following step (3) were suspended in 10 mM sodium borate-buffered physiological saline containing 50 µg/ml of NHS-LC-biotin to a cell density of 1 x 10⁷ cells/ml and incubated at room temperature for 15 minutes. After adding ammonium chloride to a final concentration of 10 mM to terminate the reaction, the thus treated cells were washed three times with 50 mM Tris-HCl buffer containing 150 mM of NaCl (pH 8.0, to be referred to as "TBS" hereinafter), thereby effecting biotinylation of cell surface protein.

(2) Preparation of mFas-Fc affinity column

15

A 4 mg portion of the purified chimera protein, mFas-Fc, prepared in Inventive Example 1 was dissolved in 4 ml of PBS (pH 7.4) and mixed with 2 ml of protein A-Sepharose 4B, and the mixture was incubated at 4 °C for 1 hour to effect their binding. In order to remove free protein molecules, the resin was washed three times with TBS and then once with 200 mM sodium borate solution (pH 9.0). Thereafter, the thus treated resin was incubated at room temperature for 45 minutes in 200 mM sodium borate solution (pH 9.0) containing dimethylpimelimidate (DMP) to effect covalent binding of mFas-Fc to the resin.

(3) Purification of Fas ligand

The d10S subline, d10S-12, obtained by 12 times of repetition of the procedure of Inventive Example 2 was cultured at 37 °C using 10 roller bottles containing 10% FCS-containing D-MEM further supplemented with 50 nM of 2-mercaptoethanol and 20 mM HEPES (pH 7.4). When the cell density reached 2 x 10⁵ cells/ml, 10 ng/ml of PMA and 500 ng/ml of ionomycin were added and the culturing was continued for additional 4 hours.

After completion of the culturing, the cell suspension was subjected to 20 minutes of centrifugation at 250 x g to recover the resulting pellet which was subsequently washed three times with PBS and then once with TBS. The thus washed pellet was stored at -80 °C for use in the following membrane fraction preparation. A portion of the pellet was also used for the biotinylation of cell surface protein carried out in the above step (1).

The frozen cell pellet was added to 4 volumes of 0.3 M sucrose solution containing 1 mM p-aminophenyl methanesulfonyl fluoride hydrochloride (APMSF), 1 µg/ml of pepstatin, 1 µg/ml of leupeptin and 0.02% NaN₃ and, using Ultra-Turrax T25 (Janke & Kunkel, Staufen), homogenized at blue position for 2 minutes on an ice bath.

Nuclei and un-homogenizd cells were removed by 20 minutes of centrifugation at 1,000 x g and at 4 ° C. The resulting supernatant fluid was then subjected to 90 minutes of centrifugation at 100,000 x g and at 4 ° C to obtain a membrane fraction. The thus obtained membrane fraction was dissolved in 40 ml of a lysis buffer (TBS containing 1% NP-40, 1 mM APMSF, 1 μg/ml of pepstatin and 1 μg/ml of leupeptin), and the solution was shaken overnight at 4 ° C to effect solubilization. The thus solubilized membrane fraction was centrifuged at 100,000 x g for 60 minutes at 4 ° C, and the resulting supernatant fluid was stored at -80 ° C. The aforementioned cells whose cell surface protein was biotinylated were also treated in the same manner and stored at -80 ° C.

A 100 ml portion of the membrane fraction solubilized to be used as a tracer of Fas ligand was mixed with 10 ml of the solubilized membrane fraction of the biotinylated cells. The resulting mixture was applied to an mFas-Fc column (1.4 ml) which has been equilibrated in advance with TBS containing 1% NP-40.

The column was washed with 50 ml of TBS containing 1% NP-40 and 50 ml of TBS containing 0.1% NP-40 and then elution of Fas ligand was carried out with 50 mM Tris-HCl buffer (pH 8.0) containing 1 M NaCl and 0.1% NP-40.

The eluates were collected in 1 ml fractions, and a 10 µl portion of each fraction was subjected to SDS-PAGE and then transferred on a PVDF membrane. The biotinylated protein was stained by allowing it to react with HRPO-labeled streptoavidin and detected by ECL system (Amersham) in accordance with the manufacturer's instructions.

Fractions containing 40 kD biotinylated Fas ligand were pooled and incubated overnight at 4 °C together with 10 µl of ConA-agarose beads (EY Laboratories). After 4 times of washing with TBS containing 0.1%

NP-40, Fas ligand was eluted with 200 μl of PBS containing 0.1% NP-40 and 2 M α -methylmannoside to obtain purified Fas ligand.

(4) SDS-polyacrylamide gel electrophoresis

The purified Fas ligand obtained in the above step (3) was subjected to electrophoresis using a 10 to 20% gradient polyacrylamide gel containing 0.1% SDS, stained using a silver staining kit (Wako Pure Chemical Industries), transferred on a PVDF membrane and then detected by the aforementioned ECL system. As shown in Fig. 13, the purified Fas ligand was detected as a single band of about 40 kD in molecular weight by both silver staining and ECL system under non-reducing conditions.

The results are shown in Fig. 13. In the drawing, the lane 1 shows results of the silver staining and the lane 2 shows the detection results by the ECL system.

(5) Cytotoxic activity

15

Cytotoxic activity of the purified Fas ligand was measured in accordance with the procedure of Inventive Example 8. In this case, however, the purified Fas ligand obtained in the above step (3) was used instead of the d10S effector cells and the COS cells transfected with pTN24-15, and the cytotoxic activity was measured using the specific cytolysis ratio on the W4 and WR19L target cells as an index. As shown in Fig. 14, cytotoxic activity was not found against WR19L cells which do not express Fas antigen, but a concentration-dependent cytotoxic activity was found against the Fas antigen-expressing W4 cells.

(Inventive Example 11) Screening using a part of rat Fas ligand DNA

(1) Screening of human chromosomal DNA library

Indicator cells (*E. coli* strain VCS257) were infected with a human (placental) chromosomal DNA phage library (EMBL3 SP6/T7, Clontech), mixed with soft agar and overlaid on agar plates. The overlaid plates were incubated overnight at 37 °C to effect formation of phage plaques. After cooling at 4 °C for about 4 hours, the phage particles were transferred on nitrocellulose filters.

Separately from this, PCR was carried out using the plasmid pTN24-15 obtained in Inventive Example 4 as a template, a sequence (AGAACTCCGTGAGTTCACCA) as a sense primer 4 (SEQ ID NO: 43, SEQ ID NO: 44) and a sequence (CAATATTCCTGGCATCCATG) as an antisense primer 4, thereby effecting amplification of a cDNA fragment which encodes the extracellular domain of rat Fas ligand cDNA (nucleotide positions 400 to 967 of SEQ ID NO: 25). A probe 1 (SEQ ID NO: 45) was prepared by labeling the amplified product with ³²P using a random primer labeling kit (Boehringer-Mannheim) in accordance with the procedure of Inventive Example 6. In the same manner, a 5'-end sequence of SEQ ID NO: 25, namely nucleotide positions 43 to 233, was amplified by PCR and labeled with ³²P to prepare a probe 2 (SEQ ID NO: 46).

The nitrocellulose filters obtained above and the thus prepared each probe was subjected to hybridization by slightly modifying the method of Shaw et al. (Nucleic Acids Res., vol. 11, pp. 555 - 573, 1983). That is, the filters were washed overnight at $65 \, ^{\circ}$ C. in $3 \times SSC$ containing 0.1% SDS and then subjected to 5 hours of prehybridization at $42 \, ^{\circ}$ C in $5 \times SSC$ containing 50% formamide, $5 \times Denhardt$ solution, 0.1% SDS and 250 µg/ml of denatured salmon sperm DNA. Next, the aforementioned each probe $(1.1 \times 10^6 \text{ cpm/ml})$ was added to $5 \times SSCP$ containing 50% formamide, $1 \times Denhardt$ solution, 0.1% SDS, $100 \times Deg/ml$ of denatured salmon sperm DNA and $10\% \times Deg/ml$ of denatured salmon sperm DN

(2) Analysis of positive clones -- 1

Phage DNA fragments were prepared from 2 clones, $\lambda hFL4$ and $\lambda hFL7$, selected from the positive clones obtained by the hybridization with the probe 1, in accordance with a known method (for example, see Sambrook J. et al., Molecular Cloning: a Laboratory Manual, 2nd. ed., Cold Spring Harbor Laboratory, New York, 1989). The clones $\lambda hFL4$ and $\lambda hFL7$ respectively contained human chromosomal DNA fragments of 18 kbp and 17 kbp, and results of their restriction enzyme mapping revealed that they have a mutually overlapped area.

A DNA fragment (SEQ ID NO: 47) corresponding to the nucleotide positions of 524 to 967 of SEQ ID NO: 25 was prepared from the plasmid pTN24-15 obtained in Inventive Example 4 and labeled with ³²P in accordance with the procedure of Inventive Example 6 to be used as a probe. The clones λhFL4 and λhFL7 were digested with several restriction enzymes and subjected to Southern hybridization using the just obtained probe 3. As the result, a 2.8 kbp *Hind*III fragment in the clones λhFL4 and λhFL7 hybridized with the probe 3.

DNA was prepared from the clone λhFL4 and digested with *HindIII*. The thus obtained 2.8 kbp fragment was inserted into *HindIII*-digested pBluescript KS(+), and the resulting plasmid was named pBL-hFL4H. When DNA sequence of the plasmid pBL-hFL4H was analyzed using a DNA sequencer (Model 370A, Perkin-Elmer Japan), it was confirmed that this plasmid contains a DNA sequence which encodes C-terminal side 130 amino acid residues of the extracellular domain of the human Fas ligand. The results are shown in Fig. 15 and SEQ ID NO: 26. In Fig. 15, a region until the 12th position counting from the 5'-end is an intron, the exon moiety starts from the 13th position G, and the sequence TAA from the 405th to 407th positions is a termination codon.

This nucleotide sequence was compared with the nucleotide sequence of pTN24-15 analyzed in Inventive Example 5, and amino acid residues and bases of rat Fas ligand which were different from those of the human Fas ligand were underlined in Fig. 15. The confirmed moiety of sequence showed high homology with the nucleotide sequence of 514th to 910th positions of SEQ ID NO: 25; 86.7% homology in the nucleotide sequence and 81.5% homology in the amino acid sequence.

A transformant, *E. coli* DH10B(pBL-hFL4H), obtained by transforming an *E. coli* strain with the plasmid pBL-hFL4H has been deposited in National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology, and has been assigned the designation as FERM P-14014, which was subsequently transferred to the International Depository Authority on October 27, 1994, as FERM BP-4849.

5 (3) Analysis of positive clones -- 2

Phage DNA was prepared in the same manner from a clone, λhFL5, selected from the positive clones obtained by the hybridization with the probe 2. It was confirmed that this clone contains a chromosomal DNA fragment of 18 kbp. DNA was prepared from the clone λhFL5 and digested with *Bam*Hl. The thus obtained fragment of 4.4 kbp was introduced into *Bam*Hl-digested pBluescript KS(+), and the resulting plasmid was named pBL-hFL5B1. When DNA sequence in the plasmid pBL-hFL5B1 was analyzed using a DNA sequencer, it was confirmed that this plasmid contains a DNA sequence which encodes 130 amino acid residues including the cytoplasmic domain of the human Fas ligand. By comparing the thus obtained nucleotide sequence with the nucleotide sequence of pTN24-15, the promoter, intron and exon regions were determined.

The results obtained in the above steps (2) and (3) are shown in Figs. 16 to 18. In these drawings, a portion indicated by ---- is an unidentified nucleotide sequence. The chromosomal gene for the human Fas ligand comprises 4 exons. All the splicing donor and acceptor sites were confirmed to the GT----AG rule (Padgett et al., Annu. Rev. Biochem. vol. 55, pp. 1119 - 1150, 1986). Further flanking sequences are in good agreement with favored nucleotide frequencies noticed in other split genes.

(Inventive Example 12) Cloning and expression of human Fas ligand-encoding cDNA

(1) Cloning of human Fas ligand cDNA by PCR

45

Firstly, lymphocytes collected from human peripheral blood were suspended to a cell density of 2 x 10^6 cells/ml in RPMI 1640 medium (NISSUI PHARMACEUTICAL) containing 10% FCS, $50~\mu\text{M}~\beta$ -mercaptoethanol and 20 ng/ml of IL-2 and cultured overnight at 37°C . Next, ConA was added to a final concentration of $5~\mu\text{g}/\text{ml}$, and the culturing was continued for 4 days at 37°C . Dead cells were removed by a density gradient centrifugation using HistoPak 1083 (Sigma Chemical), and poly (A) RNA was prepared using a mRNA preparing kit (Pharmacia). Synthesis of single-stranded cDNA and PCR were carried out in the following manner in accordance with the method of Kawasaki E.S. et al. (Amplification of RNA in PCR Protocols, A Guide to Methods and Amplifications, ed. by M.A. Innis et al., Academic Press, San Diego, pp. 21 - 27, 1990).

Firstly, a sense primer 5 (GCTCTAGACTACAGGACTGAGAAGAT) (SEQ ID NO: 48) and an antisense primer 5 (GCTCTAGAACATTCTCGGTGCCTGTAAC) (SEQ ID NO: 49) were prepared. This sense primer contains an upstream region of the ATG initiation codon and a *Xbal* site (GCTCTAGA) at 5'-end. On the other hand, the antisense primer contains a downstream region of the TAA termination codon and a

Xbal site (GCTCTAGA) at 5'-end.

To 1 μg of the poly (A) RNA were added 50 ng of random hexamers and 200 units of MMLV RNase H⁻ reverse transcriptase (Gibco BRL) and reverse transcriptation reaction was carried out. A 2.0 μI portion of the resulting reaction solution was diluted with 100 μI of a PCR buffer containing 100 pmol of the sense primer and the same amount of the antisense primer, 4xdNTP and Taq DNA Polymerase. PCR was carried out using DNA Thermal Cycler (Perkin-Elmer) by 20 cycles of the reaction, each cycle comprising incubation at 94 °C for 1 minute, 55 °C for 2 minutes and 72 °C for 3 minutes.

The thus obtained PCR product was digested with a restriction enzyme Xbal and then isolated using a 1% agarose gel (Low Gel Temperature, BioRad). A DNA fragment of about 970 bp was recovered from the gel and inserted into the Xbal site of pBluescript II, and the resulting plasmid was named pBX-hFL1. DNA sequence in the plasmid pBX-hFL1 was determined using a DNA sequencer. It was confirmed that the nucleotide sequence of the 970 bp DNA fragment contained in this plasmid coincides with the chromosomal gene sequence obtained in Inventive Example 11. The results are shown in SEQ ID NO: 31 and Figs. 19 and 20. It was found that, though the human Fas ligand does not have a signal sequence at the N-terminal side similar to the case of the rat Fas ligand, it is a type II membrane protein because it contains 22 hydrophobic amino acid residues in a central region of its protein molecule. The cytoplasmic domain comprises 80 amino acid residues starting from Met, and 32 of the 80 residues are proline. The C-terminal extracellular domain comprises 179 amino acid residues and contains 3 N-glycosylation sites (Asn-x-Ser/Thr).

A transformant, *E. coli* DH10B(pBX-hFL1), obtained by transforming an *E. coli* strain DH10B with the plasmid pBX-hFL1 in accordance with the Hanahan's method (op.cit.) has been deposited in National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology, and has been assigned the designation as FERM P-14225, which was subsequently transferred to the International Depository Authority on October 27, 1994, as FERM BP-4850.

(2) Introduction into COS cells

25

35

55

The 970 bp Xbal DNA fragment obtained in the above step (1) was inserted into the Xbal site of an animal cell expression vector pEF-BOS (Mizushima & Nagata, Nucleic Acids Res., vol. 18, p.5322, 1990), and the resulting plasmid was named pEX-hFL1. Thereafter, COS-7 cells were inoculated into D-MEM medium containing 10% FCS in cell density of 2 x 10⁵ cells per one Petri dish of 10 cm in diameter, and 5 µg of the plasmid pEX-hFL1 was introduced into the cells to obtain a transformant named COS/pEX-hFL1.

(3) Cytotoxic activity of transformant

Cytotoxic activity of recombinant cells was measured in the same manner as described in Inventive Example 8, using the COS-7 cells transformed in the above step (2) as the effector cells and 10⁵ cells of WR19L or WC8A as the target cells. The WC8A is a transformant which acquired human Fas antigenexpressing ability through the transformation of mouse WR19L cells (Itoh N. et al., J. Immunol., vol. 151, pp. 621 - 627, 1993).

That is, 10⁶ cells of WR19L or WC8A were labeled with ⁵1Cr by culturing the cells at 37 °C for 2 hours in RPMI 1640 medium containing 20 µCi of [⁵1Cr] sodium chromate (Amersham).

The thus ⁵¹Cr-labeled cells (1 x 10⁴) were mixed with COS/pEX-hFL1 cells at various mixing ratios and cultured at 37 °C for 4 hours, subsequently measuring cytotoxic activity using released ⁵¹Cr as an index. As shown in Fig. 21, the COS/pEX-hFL1 showed a cytotoxic activity against the WC8A cells in a concentration-dependent fashion. It did not induce apoptosis against WR19L. In addition, as shown in Fig. 22, the cytotoxicity of COS/pEX-hFL1 was inhibited by the addition of the chimera protein containing the extracellular domain of human Fas antigen (hFas-Fc) or the chimera protein containing the extracellular domain of mouse Fas antigen (mFas-Fc) prepared in Inventive Example 1, but was not inhibited by the addition of a soluble type human TNF receptor (hTNFRβ-Fc).

On the basis of the above results, it was confirmed that the protein encoded by the 970 bp cDNA isolated in the above step (1) is a Fas ligand which induces apoptosis by binding to the Fas antigen.

(Inventive Example 13) Isolation of mouse Fas ligand chromosomal gene

Indicator *E. coli* cells were infected with a mouse chromosomal DNA library (Stratagene) which has been prepared by introducing 129/Sv mouse chromosomal DNA into lambda FiX II vector. The thus infected cells were mixed with soft agar and overlaid on agar plates to obtain 1.3 x 10⁶ phage plaques. After cooling

at 4 °C for about 4 hours, the phage particles were transferred on nitrocellulose filters.

Separately from this, PCR was carried out using the plasmid pTN24-15 obtained in Inventive Example 4 as a template, a sequence (AGAACTCCGTGAGTTCACCA) as a sense primer 4 (SEQ ID NO: 43) and a sequence (CAATATTCCTGGCATCCATG) as an antisense primer 4 (SEQ ID NO: 44), thereby effecting amplification of a cDNA fragment which encodes the extracellular domain (nucleotide positions 400 to 967 of SEQ ID NO: 25). A probe 3 was prepared by labeling the amplified product with ³²P using a random primer labeling kit (Boehringer-Mannheim) in accordance with the procedure of Inventive Example 6. In the same manner, a 5'-end side sequence of SEQ ID NO: 25, namely nucleotide positions 43 to 233, was amplified by PCR and labeled with ³²P to prepare a probe 4.

The nitrocellulose filters obtained above and each of the thus prepared probes 3 and 4 were subjected to hybridization. The hybridization was carried out under mild conditions similar to the case of Inventive Example 16. That is, after 18 hours of hybridization at 33 $^{\circ}$ C, the filters were washed twice with 2 x SSCP containing 0.1% SDS at room temperature and then with 0.3 x SSCP containing 0.1% SDS at 37 $^{\circ}$ C. By subjecting the thus treated filters to autoradiography, 2 positive clones were obtained (λ MFL5 and λ MFL18). Each plaque of the positive clones was isolated and subcloned into pBluescript IIKS(+) (Stratagene) to prepare a restriction enzyme map of the inserted mouse chromosomal DNA fragment and determine its nucleotide sequence using a DNA sequencer.

Preparation of the restriction enzyme map of each of these 2 clones and analysis of the clones by Southern hybridization revealed that the clones λ MFL5 and λ MFL18 respectively have 5' and 3' regions of the Fas ligand chromosomal DNA. In addition, when nucleotide sequences including the promoter and the region corresponding to the rat Fas ligand cDNA were determined, the thus determined nucleotide sequence showed high homology with that of the rat Fas ligand cDNA, thus confirming that the cloned λ DNA contains the mouse Fas ligand gene.

Nucleotide sequence of the promoter, exon and 3' flanking regions of the mouse Fas ligand gene is shown in Figs. 23 and 24. The mouse Fas ligand gene contains an open reading frame of 837 bp starting from the ATG initiation codon 107 bp downstream from the TATA box, which encodes 279 amino acid residues (molecular weight of the amino acid moiety, 31,440). Similar to the case of the rat Fas ligand, the mouse Fas ligand does not have a signal sequence in its N-terminal side, but contains 22 hydrophobic amino acid residues in the central region of the protein molecule. Thus, it was revealed that the mouse Fas ligand is a type II membrane protein. Its cytoplasmic domain consists of 78 amino acid residues of which 25 are proline residues. Its C-terminal extracellular domain consists of 179 amino acid residues contains 5 N-glycosylation sites (Asn-X-Ser/Thr).

Also, it was confirmed that the mouse Fas ligand cDNA has high homology with the rat Fas ligand cDNA; 90.6% in nucleotide sequence of coding region, 91.4% in amino acid sequence and 84.5% in nucleotide sequence of 3' noncoding region.

(Inventive Example 14) Cloning of mouse Fas ligand-encoding cDNA by PCR and expression thereof

(1) Preparation of plasmid pBL-MFLW4

Splenocytes of a wild type (C3H+/+) mouse were suspended to a cell density of 2 x 10⁶ cells/ml in RPMI 1640 medium (NISSUI PHARMACEUTICAL) containing 10% FCS, 50 μM β-mercaptoethanol, 1.5 μg/ml of ConA and 20 ng/ml of IL-2 and cultured for 2 days at 37 °C. After 4 hours of treatment with 10 ng/ml of PMA and 500 ng/ml of ionomycin, dead cells were removed by a density gradient centrifugation using HistoPak 1083 (Sigma Chemical), and poly (A) RNA was prepared using a mRNA preparing kit (Pharmacia). Synthesis of single-stranded cDNA and PCR were carried out in the following manner in accordance with the method of Kawasaki E.S. et al. (Amplification of RNA in PCR Protocols, A Guide to Methods and Amplifications, ed. by M.A. Innis et al., Academic Press, San Diego, pp. 21 - 27, 1990).

Firstly, a sense primer 6 (GCTCTAGAGAGAGAGAACCCTTTCCTG) (SEQ ID NO: 50) and an antisense primer 6 (GCTCTAGAATATTCCTGGTGCCCATGAT) (SEQ ID NO: 51) were prepared. This sense primer contains an upstream region of the ATG initiation codon and a *Xbal* site (GCTCTAGA) at 5'-end. On the other hand, the antisense primer contains a downstream region of the TAA termination codon and a *Xbal* site (GCTCTAGA) at 5'-end.

To 1 μ g of the poly (A) RNA were added 50 ng of random hexamers and 200 units of MMLV RNase H⁻⁻ reverse transcriptase (Gibco BRL) and reverse transcriptation reaction was carried out. A 1.0 μ l portion of the resulting reaction solution was diluted with 100 μ l of a PCR buffer containing 100 pmol of the sense primer and the same amount of the antisense primer, 4xdNTP and Taq DNA Polymerase. PCR was carried out using DNA Thermal Cycler (Perkin-Elmer). The thus obtained PCR product was digested with a

restriction enzyme Xbal and then isolated using a 1% agarose gel (Low Gel Temperature, BioRad). A DNA fragment of about 940 bp was recovered from the gel and inserted into the Xbal site of pBluescript IIKS(+), and the resulting plasmid was named pBL-MFLW4. DNA sequence in the plasmid pBL-MFLW4 was determined using a DNA sequencer. It was confirmed that the plasmid pBL-MFLW4 contains the nucleotide sequence of SEQ ID NO: 32, and said nucleotide sequence coincides with the sequence of the chromosomal gene obtained in Inventive Example 13.

A transformant, *E. coli* DH10B(pBL-MFLW4), obtained by transforming *E. coli* DH10B with the plasmid pBL-MFLW4 in accordance with the Hanahan's method (op.cit.) has been deposited in National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology, and has been assigned the designation as FERM P-14226, which was subsequently transferred to the International Depository Authority on October 27, 1994, as FERM BP-4851.

(2) Introduction into COS cell

The 940 bp Xbal fragment obtained in the above step (1) was inserted into the Xbal site of an animal cell expression vector pEF-BOS (Mizushima & Nagata, 1990), and the resulting plasmid was named pEF-MFLW4. Thereafter, COS-7 cells were inoculated into D-MEM medium containing 10% FCS in an inoculum size of 2 x 10^6 cells per one Petri dish of 10 cm in diameter, and 5 μ g of the plasmid pEF-MFLW4 was introduced into the cells by means of the DEAE-dextran method (Fukunaga, 1990).

(3) Cytotoxic activity of transformant

20

40

Cytotoxic activity of recombinant cells was measured in the same manner as described in Inventive Example 8, using the transformed COS cells (COS/pEF-MFLW4F) obtained in the above step (2) as the effector cells and 10⁶ cells of WR19L or W4 as the target cells. The W4 is a transformant which acquired mouse Fas antigen-expressing ability through the transformation of mouse WR19L cells. That is, 10⁶ cells of WR19L or W4 were labeled with ⁵¹Cr by culturing the cells at 37 °C for 2 hours in RPMI 1640 medium containing 20 µCi of [⁵¹Cr] sodium chromate (Amersham).

The thus ⁵¹Cr-labeled cells (1 x 10⁴) were mixed with COS/pEF-MFLW4F cells at various mixing ratios and cultured at 37 °C for 4 hours, subsequently measuring cytotoxic activity using released ⁵¹Cr as an index. The results are shown in Fig. 25. As shown in Fig. 25, the COS/pEF-MFLW4F cells showed a cytotoxic activity against the W4 cells in a concentration-dependent fashion, but did not induce apoptosis against WR19L cells. The results are shown in Fig. 25. As shown in Fig. 21, the COS/pEF-MFLW4F cells also showed a cytotoxic activity against the WC8A cells in a concentration-dependent fashion. In addition, the cytotoxicity of COS/pEF-MFLW4F cells was inhibited by the addition of 20 μg/ml of the chimera protein containing the extracellular domain of mouse Fas antigen (mFas-Fc) prepared in Inventive Example 1, but was not inhibited by the addition of the soluble type human TNF receptor (hTNFRβ-Fc).

On the basis of the above results, it was confirmed that the protein encoded by the 940 bp cDNA isolated in the above step (1) is a Fas ligand which induces apoptosis by binding to the Fas antigen.

(Inventive Example 15) Production of monoclonal antibody

(1) Synthesis of peptide and preparation of immunizing antigen

Four peptides were synthesized based on the amino acid sequence determined in Inventive Example 12. Peptide (1) (LVMMEGKMMSY) (SEQ ID NO: 52) was synthesized using a Fmoc method-aided peptide synthesis kit (Kokusan Kagaku) in accordance with the manufacturer's instructions, released from the used resin by deprotection and then treated with ether to obtain 275.7 mg of crude peptide. Next, a 10 mg portion of the crude peptide was dissolved in 5% aqueous ammonia and subjected to desalting using Sephadex G10.

The thus obtained solution was subjected to purification using a reverse phase HPLC column (CAPCELLPAK C18, 120 Å, 5 μ m, 4.6 mm x 250 mm, Shiseido), and the resulting eluats were freeze-dried to obtain purified peptide.

Peptide (2) (KSNSRSMPLEWEDTYGIVLL) (SEQ ID NO: 53), peptide (3) (SKYPQDLVMMEGKMMS) (SEQ ID NO: 54) and peptide (4) (LSLVNFEESQTFF) (SEQ ID NO: 55) were obtained by requesting their synthesis to Fujiya Bioscience Laboratory.

The thus obtained peptides were linked to keyhole limpet hemocyanin (KLH: Pierce Chemical) and cationic BSA (Pierce Chemical) in the following manner to be used as immunizing antigens.

Each of the KLH and cationic BSA was dissolved in distilled water to prepare a 10 mg/ml solution. Each of the peptides was dissolved in distilled water or 5% aqueous ammonia to prepare a 1 mg/ml solution. The KLH was mixed with each peptide at a mixing ratio of 1:100, and the cationic BSA at a ratio of 1:10, and the resulting mixtures were adjusted to pH 5 with hydrochloric acid. Next, a water soluble carbodiimide (1-ethyl-3-(3-dimethylaminopropyl)-carbodiimide hydrochloride, Dojin Laboratories) was added to the mixture in an amount of 1 mg/mg KLH or cationic BSA and stirred at room temperature for 4 hours. The reaction mixture was purified by Sephadex G25 (Pharmacia), and the first eluate was used as the administration antigen.

(2) Immunization and production of antiserum

10

A 100 µg portion of the immunizing antigen prepared in the above step (1) was mixed with the same amount of Freund's complete adjuvant and administered to Balb/c or ddy mice intraperitoneally (5 to 6 weeks of age, female). After 1 week of the first administration, the same amount of the antigen was mixed with Freund's incomplete adjuvant and administered intraperitoneally. The booster was further repeated twice at one-week intervals. One week thereafter, 20 µg of the immunizing antigen was diluted with physiological saline and administered by intravenous injection. Cell fusion was carried out 2 days after the final administration. After 2 times of the administration, antiserum was obtained by collecting blood from the ophthalmic vein and separating serum.

(3) Measurement of the reactivity of antiserum with peptide

A 2.5% glutaraldehyde solution was dispensed into wells of Amino Plate (Sumitomo Bakelite) in 70 µl portions and allowed to stand still for 1 hour at room temperature, subsequently discarding the liquid contents. A 50 µl portion of each peptide solution diluted to 5 µg/ml with 0.076 M PBS (pH 6.4) was added to each well of the thus treated plate and incubated at 37 °C for 1 hour. The plate was cooled with ice water and then washed 5 times with ion-exchanged water. Thereafter, 0.2% gelatin solution in PBS was dispensed into wells of the resulting plate in 100 µl portions and allowed to stand still for 30 minutes to effect blocking.

Next, each antiserum was diluted 500 times with PBS and dispensed in 50 µl portions into the wells. After 1 hour of reaction at 37°C, the plate was washed twice with physiological saline containing 0.005% Tween 20 (to be referred to as "washing solution" hereinafter). A peroxidase-labeled anti-mouse immunoglobulins antibody (DAKO) was diluted 2,000 times with PBS containing 0.25% gelatin and added to the washed plate. After 1 hour of reaction at 37°C, the plate was washed 5 times with the washing solution. Thereafter, McIlvaine buffer solution (pH 5.0) containing 3 mg/ml of o-phenylene diamine and 0.027% hydrogen peroxide was dispensed into wells of the thus treated plate in 50 µl portions, and the reaction was carried out for 10 minutes at room temperature.

The reaction was terminated by adding $50 \, \mu$ l of 2 N sulfuric acid to each well and then absorbance at 492 nm was measured. As the result, all of the tested antisera showed reactivity with the immunizing peptide.

(4) Production of monoclonal antibody

The immunized mouse obtained in the above step (2) was sacrificed to excise the spleen which was subsequently sliced, passed through a stainless steel mesh and then suspended in RPMI 1640 medium to obtain a splenocyte suspension. The thus obtained splenocytes were mixed with mouse myeloma cells (P3X63Ag8U1) at a mixing ratio of 10:1, and the mixture was subjected to 8 minutes of centrifugation at 1,400 rpm. To the resulting precipitate was quickly added 0.5 ml of RPMI 1640 containing 42.5% polyethylene glycol 1540 and 15% dimethyl sulfoxide. After 1 minute of vigorous shaking, 10 ml of RPMI 1640 was gradually added to the cells, and the resulting mixture was subjected to 5 minutes of centrifugation at 800 rpm.

The thus obtained precipitate was suspended in HAT medium (RPMI 1640 medium supplemented with 1 \times 10⁻⁴ M hypoxanthine, 4 \times 10⁻⁷ M aminopterin, 1.6 \times 10⁻⁵ M thymidine and 10% FCS) to a final cell density of 2 \times 10⁵ cells/ml, and the suspension was dispensed into wells of a 96 well microplate in 0.2 ml portions. Half of the medium was exchanged with fresh medium every 2 to 3 days, and the medium was then exchanged entirely with HT medium (RPMI 1640 medium supplemented with 1 \times 10⁻⁴ M hypoxanthine, 1.6 \times 10⁻⁵ M thymidine and 10% FCS).

When growth of hybridoma cells was observed, screening was carried out by means of ELISA. That is, a 96 well plate to which the peptide prepared in Inventive Example 15 (1) has been immobilized was washed twice with the aforementioned washing solution, and a 100 µl portion of each culture supernatant

which has been diluted 10 times with PBS containing 0.25% gelatin was added to each well of the thus washed plate and allowed to undergo 2 hours of reaction at room temperature. After completion of the reaction, the plate was washed 5 times with the washing solution, and 50 μ l of a peroxidase-labeled rabbit anti-mouse lgs antibody (DAKO) which has been diluted 2,000 times with PBS containing 0.25% gelatin was added as the second antibody to each well of the thus washed plate.

After 2 hours of reaction at room temperature, the plate was washed 5 times with the washing solution, and 0.1 M McIlvaine buffer solution (pH 5.0) containing 3 mg/ml of o-phenylene diamine and 0.027% hydrogen peroxide was dispensed into wells of the thus treated plate in 100 µl portions. After 10 minutes of enzyme reaction at room temperature, the reaction was terminated by adding 100 µl of 2 N sulfuric acid to each well and then absorbance at 492 nm was measured. Hybridomas in wells which showed positive by ELISA were diluted with RPMI 1640 containing 10% FCS at such a ratio that each well of 96 well microplate contained 2, 1 or 0.5 cell.

Thymocytes of Wistar rat were inoculated into each well of the plate as feeder cells to carry out cloning. Wells, each containing a single cell colony, were selected by observing them under a microscope, and culture supernatants in the selected wells were screened by the ELISA procedure of the above step (3) to obtain a hybridoma capable of producing the monoclonal antibody of interest.

(5) Confirmation of reactivity by western blotting

Reactivity of the antiserum obtained in the above step (2) (immunized with the antigen prepared using the peptide (2), lot. 19-3) and the monoclonal antibody obtained in the above step (4) (immunized with the antigen prepared using the peptide (2), F864-5-1) with human Fas ligand was confirmed by western blotting. As samples, COS cells transfected with a vector containing the sequence of the human Fas ligand expressed in COS cells in Inventive Example 12 or of the mouse Fas ligand expressed in Inventive Example 14 or containing no Fas ligand sequence were used.

Firstly, about 1 x 10⁴ of each of the transformed COS cells were mixed with 9 μ I of 50 mM Tris-HCl buffer (pH 7.5) containing 150 mM NaCl, 1% NP-40, 0.1% sodium deoxycolate, 0.1% SDS and 0.2 U/ml of aprotinin and then with the same volume of 0.25 M Tris-HCl buffer (pH 6.8) containing 2% SDS, 30% glycerol, 10% 2-mercaptoethanol and 0.01% BPB (Bromophenol Blue).

After 1 hour of treatment at 37 °C, SDS-polyacrylamide gel electrophoresis (4 to 20% gradient gel) was carried out, and the contents in the gel were subsequently transferred on a PVDF membrane (Millipore Corp.) under reaction conditions of 200 mA for 90 minutes at 4 °C. The resulting membrane was subjected to 2 hours of blocking at 37 °C using Block Ace (Snow Brand Milk Products).

Next, the membrane was washed twice with the washing solution (4 minutes of stirring at 37 °C) and then allowed to react for 1.5 hours at 37 °C with the antiserum 19-3 or culture supernatant of hybridoma F864-5-1 which has been diluted 500 times with Block Ace that has been diluted 5 times with PBS. After completion of the reaction, the membrane was washed twice with the washing solution and then soaked in a solution of peroxidase-labeled rabbit anti-mouse immunoglobulins antibody (Cat. No. P260, DAKO) which has been diluted 1,000 times with 5 times-diluted Brock Ace with PBS. After 1.5 hours of reaction at 37 °C, the membrane was washed 3 times with the washing solution and then twice with distilled water. Thereafter, water on the surface of the membrane was removed to carry out color development with TMB reagent (Cat. No. TM9125, SCYTK).

Results of the western blotting using the antiserum 19-3 and the monoclonal antibody F864-5-1 are respectively shown in Figs. 27 and 28. As is evident from these drawings, a band capable of reacting with the extract of the human Fas ligand-expressing COS cells was observed, while such a band was not found in the case of mouse Fas ligand and control.

(6) Confirmation of the reactivity of the monoclonal antibody with peptide (2) by blocking reaction-1

Reactivity of the monoclonal antibody obtained in the above step (4) (immunized with the antigen prepared using the peptide (2), F883-1-1) with the immunizing peptide (2) was confirmed by blocking reaction.

A 2.5% glutaraldehyde solution was dispensed into wells of Amino Plate (Sumitomo Bakelite) in 70 µl portions and allowed to stand still for 1 hour at room temperature, subsequently discarding the liquid contents. A 50 µl portion of a solution of the peptide (2) diluted to 5 µg/ml with 0.076 M PBS (pH 6.4) was added to each well of the thus treated plate and incubated at 37 °C for 1 hour. The plate was cooled with ice water and then washed 5 times with ion-exchanged water. Thereafter, PBS containing 0.2% gelatin and 0.1 M glycine was dispensed into each well of the resulting plate in 100 µl portion and allowed to stand still

for 30 minutes to effect blocking.

Separately from this, each of the aforementioned peptides (2), (3) and (4) was diluted with PBS to a concentration of 10 µg/ml to be used as a blocking antigen solution. Also, a solution containing no blocking antigen was prepared to be used as a negative control. After adding 25 µl of each of these solutions to each well of the above plate, the antibody F883-1-1 which has been diluted to 0.4 µg/ml with 0.2% gelatin-containing PBS was dispensed in 25 µl portions into the wells. After 1 hour of reaction at 37 °C, the plate was washed twice with the washing solution.

Next, a peroxidase-labeled anti-mouse immunoglobulins antibody (DAKO) was diluted 2,000 times with PBS containing 0.2% gelatin and dispensed into wells of the washed plate in 50 μ I portions. After 1 hour of reaction at 37 °C, the plate was washed 5 times with the washing solution. Thereafter, McIlvaine buffer solution (pH 5.0) containing 3 mg/ml of o-phenylene diamine and 0.027% hydrogen peroxide was dispensed into wells of the thus treated plate in 50 μ I portions, and the reaction was carried out for 10 minutes at room temperature. The reaction was terminated by adding 50 μ I of 2 N sulfuric acid to each well and then absorbance at 492 nm was measured. The results are shown in Fig. 29.

In Fig. 29, absorbance of a well to which the blocking antigen was not added (negative control) was taken as 100, and relative absorbance in each of other wells was shown.

As is evident from Fig. 29, it was confirmed that the reactivity of the F883-1-1 antibody with the antigen peptide is inhibited only when the peptide (2) is used as a blocking peptide.

(7) Confirmation of the reactivity of the monoclonal antibody with the peptide (3) by blocking reaction-2

Reactivity of the IgM monoclonal antibody produced in the above (4) (antibody F897-1-2 produced by hybridoma F897-1-2, which has been produced from the spleen cell of the mouse immunized with the antigen produced using the peptide (2) and the myeloma cell) with the immunizing antigen peptide (3) (peptide (3)) was confirmed by means of blocking reaction.

First, peptide (3) was labeled with peroxidase in accordance with Nakane et al., Immunofluorescence and Related Staining Techniques, W. Knapp, K. Holubar and G. Wick eds., 1978) as described below.

6 mg of peroxidase (RZ3.11, Toyobo Co., Ltd.) was dissolved in 1.5 ml of distilled water. To the solution was added 0.3 ml of 0.1M sodium m-periodate in distilled water, and the solution was allowed to stand at room temperature for 15 minutes. To the solution was then added 0.3 ml of 1.5% ethylene glycol in distilled water, and the solution was allowed to stand for 20 minutes. The resulting solution was dialyzed against 0.001M acetate buffer, pH 4.4 at 4 °C overnight.

To 159 μ I of the resulting activated peroxidase solution (corresponding to 500 μ g of peroxidase) was added 9 μ I of 1M carbonate buffer solution, pH 9.5, and then, 428 μ I of the solution of peptide (3) which had been prepared by dissolving the peptide (3) in distilled water to a concentration of 1 mg/mI (the amount of the peptide (3) being 20 times the molar amount the peroxidase), and the solution was allowed to react at 25 °C for 2 hours. To the solution was added 15 μ I of sodium borohydride solution prepared by dissolving the sodium borohydride in 0.01M carbonate buffer solution, pH 9.5 to 4 mg/mI, and the solution was allowed to stand at 4 °C for 2 hours. To the solution was further added 25 μ I of 0.2M glycine in distilled water, and the solution was allowed to stand at room temperature for 1 hour. The solution was then dialyzed against 0.076M PBS, pH 6.4 at 4 °C overnight, and to the resulting solution of peroxidase labeled peptide (3) was added an equal amount of glycerol. The mixture was stored at -20 °C.

Next, 20 μg/ml anti-mouse immunoglobulins antibody (Z259, DAKO) in 0.076M PBS was dispensed into wells of an immunoplate (Maxi Sorp™, NUNC) in 50 μl portions, and the plate was incubated at 45 °C for 30 minutes. The plate was then cooled with ice water, and washed 5 times with ion exchanged water. To the wells were then dispensed PBS containing 0.2% gelatin in 100 μl portions, and the plate was kept at 4 °C overnight for blocking. After the blocking, the salted out antibody (F897-1-2) diluted to 100 times with PBS was dispensed in 50 μl portions, and the plate was incubated at 37 °C for 1 hour. The plate was then washed twice with 0.9% NaCl washing solution containing 0.005% Tween 20, and once with ion exchanged

In the meanwhile, peptide (3) was diluted with PBS to a concentration of 3 µg/ml and 10 µg/ml, respectively, and the resulting solutions were used for the blocking antigen solutions. A solution containing no blocking antigen was also prepared, and the solution was used for the negative control. To the wells of the plate were dispensed the thus prepared solutions in 25 µl portions, and then, the peroxidase-labeled peptide (3) diluted 200 times with PBS in 25 µl portions. The plate was incubated at 37 °C for 1 hour to promote the reaction. After the completion of the reaction, the plate was washed 5 times with the washing solution, and twice with the ion exchanged water. To the wells were dispensed 50 µl portions of McIlvaine buffer, pH 5.0 containing 3 mg/ml of o-phenylene diamine and 0.027% hydrogen peroxide, and the reaction

was promoted at room temperature for 5 minutes. 50 µI portions of 2N sulfuric acid were dispensed into the wells to cease the reaction, and absorbance at 492 nm was measured.

Reactivity in percentage was calculated in terms of the relative absorbance of each well by taking the absorbance of the well free from the blocking antigen (the negative control) as 100. The results are shown in Fig. 31.

As clearly shown in Fig. 31, it was confirmed that the reactivity of the antibody F897-1-2 with the antigen peptide is inhibited by the peptide (3).

(Inventive Example 16) Evaluation of apoptosis inhibition activity - 1

10

Apoptosis inhibition activity of antibody F883-1-1 produced in Inventive Example 15 was confirmed in the following manner using a Fas ligand-expressing transformant and a Fas antigen-expressing transformant

First, cell line FDC-P1 derived from a normal mouse myeloid cell was transformed with plasmid pEX-hFL1 (see Inventive Example 12), which includes cDNA coding for the human Fas ligand. FLh1 cells, which are one of the resulting clones, were incubated at 37 °C for 4 days in the presence of 5% CO₂ in RPMI 1640 medium (Gibco BRL) supplemented with 50 U/ml of mouse IL-3 (INTERGEN) and 10% FCS. After the incubation, FLh1 cells were suspended in 10% FCS-containing RPMI 1640 medium to a cell concentration of 5 x 10⁵ cells/ml, and the cell suspension was dispensed into wells of a 96 well flat bottom plate in 50 μI portions.

In the meanwhile, antibody F883-1-1 produced in Inventive Example 15 was diluted with PBS⁻ to various concentrations. The thus diluted antibody solutions were dispensed into the above-described wells in 10 µl portions, and the plate was incubated at 37 °C for 30 minutes in the presence of 5% CO₂.

Next, transformant cells WC8 capable of expressing the human Fas antigen (Itoh N. et al., J. Immunol., vol. 151, pp621-627, 1993) were suspended in 10% FCS-containing RPMI 1640 medium to a cell concentration of 6.3 x 10⁵ cells/ml, and the suspension was dispensed into the wells in 40 μl portions. After 16 hours of incubation at 37 °C in the presence of 5% CO₂, 100 μl of trypan blue was added to each well to count the number of survived cells in each well.

Fig. 30 shows apoptosis inhibition activity of antibody F883-1-1 produced in Inventive Example 15. As clearly shown in Fig. 30, apoptosis of WC8 cells induced by FLh1 is inhibited by antibody F883-1-1 in a dose-dependent manner. It should be noted that the inventors of the present application have deposited hybridoma F883-1-1, which produces monoclonal antibody F883-1-1, in National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology on August 9, 1994 (Deposit No. FERM P-14464), which was subsequently transferred to the International Depository Authority on October 27, 1994, as FERM BP-4852.

(Inventive Example 17) Evaluation of apoptosis inhibition activity - 2

Apoptosis inhibition activity of antibody F897-1-2 produced in Inventive Example 15 was confirmed as described below in accordance with the procedure of Inventive Examples 8 and 12 using the supernatant of transformant COS-1/pEX-hFL1 produced in accordance with the procedure of Inventive Example 18(3) and the human Fas antigen-expressing transformant cells WC8.

First, 10⁶ cells of WC8 were incubated in PRMI-1640 medium supplemented with 20 μ Ci [5¹Cr]sodium chromate (NEN) and 10% heat-inactivated FCS at 37 °C for 2 hours to label the cells with the ⁵¹Cr.

Next, to each well of a 96 well U-bottom plate (CORNING) were dispensed 6 μ I of the supernatant of COS-1/pEX-hFL1 to a final concentration of 3%, and 74 μ I of 10% FCS-containing RPMI 1640 medium. To each well was then dispensed 20 μ I of the dilution of antibody F-897-1-2 produced in Inventive Example 15, which has been adjusted with 0.1% BSA-containing PBS⁻ to 300 μ g/mI, to a final concentration of 30 μ g/mI. The plate was incubated at 37 °C for 30 minutes. The ⁵¹Cr-labeled WC8 cells were then dispensed at 1 x 10⁴ cells/100 μ I/well, and the plate was incubated at 37 °C for another 4 hours. After the incubation, cytotoxic activity was evaluated by using the release of ⁵¹Cr for the index.

The results are shown in Fig. 32. As clearly shown in Fig. 32, apoptosis of WC8 cells induced by the Fas ligand present in the supernatant of transformant COS-1/pEX-hFL1 was inhibited by antibody F897-1-2 in a dose-dependent manner.

It should be noted that the inventors of the present application have deposited hybridoma F897-1-2, which produces monoclonal antibody F897-1-2, in National Institute of Bioscience and Human Technology, Agency of Industrial Science and Technology on September 1, 1994 (Deposit No. FERM P-14497), which was subsequently transferred to the International Depository Authority on October 27, 1994, as FERM BP-

4853.

20

(Inventive Example 18) Expression of the extracellular domain of the human Fas ligand

5 (1) Preparation of plasmid pM1067

A sense primer 7 (CACCTGCAGAAGGAGCTGGCAGAA) (SEQ ID NO: 56) and an antisense primer 7 (AATAAGCTTGGTACCCTATTAGAGCTTATATAA) (SEQ ID NO: 57) were synthesized in a chemical synthesizer. The sense primer contains the nucleotide sequence coding for the amino acid sequence located at the N terminus of the extracellular domain of the human Fas ligand, of which amino acid sequence is shown in SEQ ID NO: 3 and Pst site (CTGCAG). The antisense primer contains SEQ containing the termination codon (TAA), HindIII site (AAGCTT), and KpnI site (GGTACC).

A 100 μ I solution containing 100 pmol each of the sense primer and the antisense primer; 50 ng of plasmid pBX-hFL1 produced in Inventive Example 12(1); 20 nmol each of dATP, dCTP, dGTP, and dTTP; and 2.5 units of pfu polymerase and 10 μ I of pfu buffer attached therewith (Stratagene) was prepared. PCR was carried out using DNA Thermal Cycler (PCR System 9600, Perkin-Elmer) by repeating 30 cycles each comprising 94 °C for 30 seconds, 55 °C for 30 seconds and 72 °C for 1 minutes. The resulting PCR product was double digested with *Pst*I and *Hind*III, and the DNA fragment was inserted between the *Pst*I site and the *Hind*III site of pUC118. The resulting plasmid was designated plasmid pM1067.

(2) Preparation of plasmid pM1070

A sense primer 8 (TGCGAATTCIACCATGCTGGGCATCTGG) (SEQ ID NO: 58) and an antisense primer 8 (AACCTGCAGGTGGAAGAGCTAAGACGTAAG) (SEQ ID NO: 59) were synthesized in a chemical synthesizer. The sense primer contains the sequence located at the 5' terminus of a sequence coding for the signal peptide of the human Fas antigen; and *EcoR*I site (GAATTC). The antisense primer contains the sequence located at the 3' terminus of a sequence coding for the signal peptide of the human Fas antigen; the nucleotide sequence coding for the N terminus of the extracellular domain of the human Fas ligand, and *Pst*I site.

A 100 μ I solution containing 100 pmol each of the sense primer and the antisense primer; 50 ng of plasmid pBLF58-1 used in Inventive Example 1(3); 20 nmol each of dATP, dCTP, dGTP, and dTTP; and 2.5 units of pfu polymerase and 10 μ I of pfu buffer attached therewith (Stratagene) was prepared, and PCR was carried out by repeating the procedure of the above (1).

The resulting PCR product was double digested with *EcoR*I and *Pst*I, and the resulting DNA fragment was inserted between the *EcoR*I site and the *Pst*I site of plasmid pM1067 produced in the above (1) to obtain plasmid pM 1250. The thus produced plasmid was double digested with *EcoR*I and *Kpn*I, and the digestion product was electrophoresed on agarose gel. A DNA fragment of about 600 bp was recovered, and the DNA was purified with QIAEX™ kit QIAGEN. The thus purified DNA fragment of about 600 bp was inserted between the *EcoR*I site and the *Kpn*I site of plasmid pM1103 that had been produced by inserting DHFR gene into plasmid pEF-BOS used in Inventive Example 14(2). The resulting plasmid was designated plasmid pM1070.

(3) Introduction into COS cells

pM1070 produced in the above (1) and pEX-hFL1 produced in Inventive Example 12(1) were respectively introduced in COS-1 cells to produce transformants COS-1/pM1070 and COS-1/pEX-hFL1 by the procedure as described below.

To 40 μ I of 10 mM Tris-HCl buffer solution (pH 7.4)/1 mM ethylenediaminetetraacetic acid (hereinafter referred to as Tris/EDTA) was added 8.1 μ g of pM1070 or pEX-hFL1. To the resulting solutions were then added 11.3 ml of D-MEM (Nissui Pharmaceutical) containing 0.2 mg/ml DEAE-dextran and 50 mM Tris-HCl, pH 7.4 to prepare DNA-DEAE-dextran mixed solutions.

The resulting DNA-DEAE-dextran mixed solutions were respectively added dropwise to a monolayer culture of COS-1 cells in 150 cm² Roux flasks that had grown to their semiconfluent stage, and the cultures were incubated at 37 °C in the presence of 5% CO₂ to produce the transformants COS-1/pM1070 and COS-1/pEX-hFL1. After 4 hours of incubation, the DNA-DEAE-dextran mixed solutions were removed, and D-MEM containing 10% FCS (IRVINE Scientific K.K.) was added to the flasks. The incubation was continued for another 48 to 96 hours, and culture supernatants were collected from the COS-1/pM1070 and COS-1/pEX-hFL1 for use in the (4) and (5) as described below.

(4) Cytotoxic activity of the transformant

The cytotoxic activity of the culture supernatants of COS-1/pM1070 and COS-1/pEX-hFL1 produced in the above (3) was evaluated as in the case of Inventive Examples 8 and 12 by using WC8A cells and W4 cells for the target cells, respectively. The evaluation was carried out as described below.

In RPMI1640 medium containing 20 µCi of [51Cr] sodium chromate (NEN) were incubated 10⁶ cells of WC8 or W4 cells at 37 °C for 2 hours to label the cells with the ⁵¹Cr.

The cell culture supernatants produced in the above (3) were added to the reaction solution containing 1 x 10⁴ ⁵¹Cr-labeled cells to a final concentration of 3% and 10%, respectively. The cultures were incubated at 37 °C for 4 hours, and cytotoxic activity was evaluated by using the release of the ⁵¹Cr for the index.

The results are shown in Figs. 33 and 34. As apparent in Figs. 33 and 34, the culture supernatants of COS-1/pM1070 and COS-1/pEX-hFL1 exhibited concentration dependent cytotoxic activity on WC8A cells and W4 cells, respectively. In Figs. 33 and 34, "Mock" designates the control.

Presence in such culture supernatants of the Fas ligand having the activity of binding with the human Fas antigen to induce apoptosis was thus confirmed.

(5) Western blotting using the culture supernatants of transformants COS-1/pM1070 and COS-1/pEX-hFL1

A rabbit antiserum capable of recognizing a part of the amino acid sequence of the human Fas ligand (PSPPPEKKELRKVAH, SEQ ID NO: 60) was prepared in accordance with a known procedure, and western blotting was carried out by using the thus prepared rabbit antiserum as descirbed below.

10 µI of the culture supernatants of transformants COS-1/pM1070 and COS-1/pEX-hFL1 produced in the above (3) were respectively mixed with 5 µI of distilled water. To such mixtures were respectively added a 5 µI of distilled water containing 4% SDS, 80% glycerol, and 0.04% BPB, or a 5 µI of distilled water containing 4% SDS, 80% glycerol, 8% DTT, and 0.04% BPB. The resulting mixtures were incubated at 37°C for 1 hour, and then, subjected to SDS-polyacrylamide gel electrophoresis on 5 to 20% gradient gel. After completing the electrophoresis, the gel was transferred to PVDF membrane (Atto K.K.) at room temperature, a 200 mA for 60 minutes, and the membrane was blocked by the solution of skim milk (Snow Brand Milk Products, Co., Ltd.) at 4°C overnight. The thus blocked membrane was washed once with PBS (by incubating at room temperature for 15 minutes), and twice with 0.1% Tween 20/PBS (by incubating at room temperature for 5 minutes).

The rabbit antiserum as described above was diluted 1,000 times with 0.5% BSA/0.1% Tween 20/PBS, and the membrane was allowed to react with the thus diluted rabbit antiserum at 37 °C for 1 hour. After the completion of the reaction, the membrane was washed twice with 0.1% Tween 20/PBS. The membrane was then immersed in a solution of peroxidase-labeled anti-rabbit immunoglobulins antibody (Cat. No. P448, DAKO) which had been diluted 1,000 times with 0.5% BSA/0.1% Tween 20/PBS, and allowed to react at room temperature for 1 hour. The membrane was washed 5 times with 0.1% Tween 20/PBS, and water on the surface was removed. The membrane was then evaluated in ECL system (Amersham).

In the case of the supernatant of COS-1/pM1070, a band was observed at about 29 kD under reduced conditions, and at about 26 kD under non-reduced conditions.

In the case of the supernatant of COS-1/pEX-hFL1, a band was observed at about 26 kD under reduced conditions, and at about 24 kD under non-reduced conditions.

The results of the western blotting under non-reduced conditions are shown in Figs. 35 and 36.

(Inventive Example 19) Inhibition of the expression of Fas ligand by antisense oligonucleotide

(1) Synthesis of antisense oligonucleotide

A phosphorothicate sense oligonucleotide of 22 nucleotides containing the nucleotide sequence (TAAAACCGTTTGCTGGGGCTGG) from 20th to 41st nucleotides in SEQ ID NO: 31 (hereinafter referred to as sense oligonucleotide S20), and a phosphorothicate antisense oligonucleotide having the complementary sequence (CCAGCCCCAGCAAACGGTTTTA) to the sense oligonucleotide S20 (hereinafter referred to as antisense oligonucleotide A41) were synthesized in accordance with a known method (SEQ ID NOS: 61 and 62). The resulting synthetic oligonucleotides were respectively dissolved in TE buffer to a concentration of 1 mM

(2) Introduction of antisense oligonucleotide into the cell

Transformant FLh1 cells expressing the human Fas ligand (see Inventive Example 16) were suspended in RPMI 1640 medium containing 10% heat-inactivated FCS, and the cell suspension was dispensed into wells of a 96 well plate (NUNC) at 2.0 x 10⁴ cells/196 μI/well.

The 1 mM solution of antisense oligonucleotide A41 produced in the above (1) was dispensed in the wells in 4 μl portions to a final concentration of 20 μM, and the plate was incubated in the presence of 5% CO₂ for 3 days to introduce the oligonucleotide into the cells.

Into the wells containing the cell suspension were also dispensed 4 µI portions of the 1 mM solution of sense oligonucleotide S20 produced in the above (1) and the TE buffer, respectively, and the plate was incubated in the presence of 5% CO₂ for 3 days. Such wells were used for the control.

(3) Evaluation of cytotoxic activity

FLh1 cells that had been incubated for 3 days in the above (2) were used for the effector cells to evaluate the cytotoxic activity on human Fas antigen-expressing transformant WC8.

The cytotoxic activity was evaluated as described below in accordance with the method used in Inventive Examples 8 and 12.

In RPMI1640 medium containing 20 µCi of [5¹Cr] sodium chromate (NEN), 10⁵ cells of WC8 were incubated at 37°C for 2 hours to label the WC8 cells with the 5¹Cr. The effector cells as described above were mixed with 1 x 10⁴ 5¹Cr-labeled cells at an E/T ratio of 3:1. The culture was incubated at 37°C for 5 hours, and cytotoxic activity was evaluated by using the release of the 5¹Cr for the index.

The results are shown in Fig. 37. As shown in Fig. 37, the FLh1 cells carrying antisense oligonucleotide A41 introduced therein exhibited an apoptosis inhibition activity on WC8 cells.

(Inventive Example 20) Inhibition of the expression of Fas ligand by antisense oligonucleotide-2.

(1) Synthesis of antisense oligonucleotides

Phosphorothioate sense oligonucleotides S50, S163, S338, S484, S714, and S905 and phosphorothioate antisense oligonucleotides A69, A184, A355, A505, A733, and A924 (SEQ ID NOS: 63 to 74) were synthesized in accordance with a known method by referring to the DNA sequence coding for the human Fas ligand (SEQ ID NO: 31).

Of the thus synthesized oligonucleotides, sense oligonucleotide S50 and antisense oligonucleotide A69 are oligonucleotides of 20 nucleotides respectively containing the nucleotide sequence (ACCAGCTGCCAT-GCAGCAGC) from 50th to 69th nucleotides in SEQ ID NO: 31, and the complementary sequence (GCTGCTGCATGGCAGCTGGT) to such sequence.

Sense oligonucleotide S163 and antisense oligonucleotide A184 are oligonucleotides of 22 nucleotides respectively cantaining the nucleotide sequence (CTGTGCCCAGAAGGCCTGGTCA) from 163rd to 184th nucleotides in SEQ ID NO: 31, and the complementary sequence (TGACCAGGCCTTCTGGGCACAG) to such sequence.

Sense oligonucleotide S338 and antisense oligonucleotide A355 are oligonucleotides of 18 nucleotides respectively containing the nucleotide sequence (CTTGGTAGGATTGGGCCT) from 338th to 355th nucleotides in SEQ ID NO: 31, and the complementary sequence (AGGCCCAATCCTACCAAG) to such sequence.

Sense oligonucleotide S484 and antisense oligonucleotide A505 are oligonucleotides of 22 nucleotides respectively containing the nucleotide sequence (AGCTGAGGAAAGTGGCCCATTT) from 484th to 505th nucleotides in SEQ ID NO: 31, and the complementary sequence (AAATGGGCCACTTTCCTCAGCT) to such sequence.

Sense oligonucleotide S714 and antisense oligonucleotide A733 are oligonucleotides of 20 nucleotides respectively containing the nucleotide sequence (CCCCAGGATCTGGTGATGAT) from 714th to 733rd nucleotides in SEQ ID NO: 31, and the complementary sequence (ATCATCACCAGATCCTGGGG) to such sequence.

Sense oligonucleotide S905 and antisense oligonucleotide A924 are oligonucleotides of 20 nucleotides respectively having the nucleotide sequence (AGAGAAGCACTTTGGGATTC) from 905th to 924th nucleotides in SEQ ID NO: 31, and the complementary sequence complementary (GAATCC-CAAAGTGCTTCTCT) to such sequence.

The resulting synthetic oligonucleotides were respectively dissolved in TE buffer to a concentration of 1 mM.

(2) Introduction of antisense oligonucleotides into the cells

First, mouse fibroblast-like cell line L929 was transformed with plasmid pEX-hFL1 (see Inventive Example 12(2)), which carries the cDNA coding for the human Fas ligand. LFLh3 cells, which are one of the resulting clones, were suspended in D-MEM supplemented with 10% FCS, and the suspension was dispensed into wells of a 6 well plate (NUNC) at 3.0 x 10⁵ cells/2.0 ml/well. The plate was incubated at 37 °C overnight in the presence of 5% CO₂.

On the next day, the oligonucleotides synthesized in the above (1) were respectively suspended in 1,000 μ l of OPTIMEM TM I (Gibco BRL) supplemented with lipofectamine (Gibco BRL) to prepare oligonucleotide-lipofectamine mixed solutions. The medium was removed and the mixed solutions were respectively added to LFLh3 cells which were incubated at 37 °C overnight in the presence of 5% CO₂. After incubating at 37 °C for 4 hours in the presence of 5% CO₂, 1,000 μ l of D-MEM supplemented with 20% heat-inactivated FCS and 1 μ M oligonucleotide was added to the culture, and the culture was incubated for another 16 hours to introduce the oligonucleotides synthesized in the above (1) respectively into the LFLh3 cells.

(3) Evaluation of cytotoxic activity

5

40

LFLh3 cells into which the oligonucleotides had been respectively introduced in the above (2) were collected, and treated in trypsin solution for 3 minutes. The cells were then used for the effector cells to evaluate the cytotoxic activity.

The cytotoxic activity was evaluated as described below in accordance with the method used in Inventive Examples 8 and 12.

In RPMI1640 medium containing 20 μ Ci of [51 Cr] sodium chromate (NEN), 10^{6} cells of WC8 were incubated at 37 $^{\circ}$ C for 2 hours to label the WC8 cells with the 51 Cr. The effector cells as described above were mixed with 1 x 10^{4} 51 Cr-labeled cells at an E/T ratio of 1:1. The culture was incubated at 37 $^{\circ}$ C for 4 hours, and cytotoxic activity was evaluated by using the release of 51 Cr for the index.

The LFLh3 cells carrying antisense oligonucleotide A69, A184, A355, A505, A733, or A924 introduced therein exhibited an apoptosis-inhibition activity on WC8 cells. Inhibition of the specific cytolysis of the antisense oligonucleotides was calculated by the following formula:

Inhibition (%) of the = {1 - (D/E)} x 100 specific cytolysis

- D: Specific cytolysis rate of LFLh3 cells carrying the antisense oligonucleotide,
- E: Specific cytolysis rate of LFLh3 cells carrying the sense oligonucleotide.

The results are shown in Fig. 38.

(Inventive Example 21) Expression of deletion mutants of the extracellular domain of the human Fas ligand in an animal cell host

Polypeptides ND38 (SEQ ID NO: 76), ND40 (SEQ ID NO: 77), ND41 (SEQ ID NO: 78), ND42 (SEQ ID NO: 79), ND43 (SEQ ID NO: 80), and CD179 (SEQ ID NO: 81), which are deletion mutants of the extracellular domain of the human Fas ligand, were expressed as described below. It should be noted that ND38, ND40, ND41, ND42, ND43 are polypeptides having the amino acid sequences of SEQ ID NO: 3 from which 38, 40, 41, 42, and 43 amino acids on the N terminus are respectively deleted. In other words, ND38, ND40, ND41, ND42, and ND43 are polypeptides respectively having the amino acid sequences of amino acid NOS: 39 to 179, 41 to 179, 42 to 179, 43 to 179, and 44 to 179 in SEQ ID NO: 3. CD179 is a polypeptide having the amino acid sequence of SEQ ID NO: 3 from which 1 amino acid on the C terminus is deleted. In other words, CD179 is a polypeptide having the amino acid sequence of amino acid NOS: 1 to 178 in SEQ ID NO: 3.

(1) Preparation of plasmid pM1081

Plasmid pM1081 is a plasmid carrying a nucleotide sequence coding for the signal peptide of the human Fas antigen and the extracellular domain of the human Fas ligand, wherein Spel and PshAl

recognition sequences have been introduced in the nucleotide sequence coding for the signal peptide of the human Fas antigen, and a *Pst*1 recognition sequence has been introduced in the nucleotide sequence coding for the human Fas ligand by means of silent mutation. The plasmid pM1081 was prepared as described below.

First, an antisense primer 9 (CTTCTGCAGGTGGAAGAGCTGAGCGACACTAGTCAGAACCAGAGG) (SEQ ID NO: 82) was synthesized. This antisense primer includes a nucleotide sequence coding for the N terminus of the human Fas ligand and the C terminus of the signal peptide of the human Fas signal; Psti site (CTGCAG); Spel site (ACTAGT); and PshAI site (GACTAGTATC).

A 100 µl solution containing 100 pmol of the resulting antisense primer; 100 pmol of the sense primer 8 (TGCGAATTCACCATGCTGGGCATCTGG, containing *EcoR*l site (GAATTC) and a sequence coding for the N terminus of the signal peptide of the human Fas antigen) used in Inventive Example 18(2); 50 ng of plasmid pBLF58-1 used in Inventive Example 1(3); and 2.5 units of pfu DNA polymerase and 10 µl of pfu buffer attached therewith was prepared. PCR was carried out by repeating the procedure of Inventive Example 18(1), and the PCR product was double digested with *EcoR*l and *Pst*l, and the digestion product was electrophoresed on agarose gel. A DNA fragment of about 70 bp was recovered, and the DNA was purified with QIAEXTM kit. The thus purified DNA fragment of about 70 bp was inserted between the *EcoR*l site and the *Pst*l site of plasmid pM1067 prepared in Inventive Example 18(1).

The resulting plasmid was examined for its nucleotide sequence, and it was then detected that 16 nucleotides were missing between the *EcoR*I site and the *Spe*I site. In order to construct the sequence between the *EcoR*I site and the *Spe*I site, a sense oligonucleotide 9 (AATTCACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTTCTGA) SEQ ID NO: 83 and an antisense oligonucleotide 10 (CTAGTCAGAACCAGAGGTAGGAGGGTCCAGATGCCCAGCATGGTG) SEQ ID NO: 84 were synthesized, and a 20 µI TE solution containing 1 nmol of the thus synthesized sense oligonucleotide and 1 nmol of the antisense oligonucleotide was prepared. The solution was heated to 95 °C for 5 minutes and gradually cooled to 16 °C to anneal the oligonucleotides to thereby obtain a double stranded DNA fragment having the *EcoR*I cleavage site and the *Spe*I cleavage site on opposite ends. The thus obtained DNA fragment was inserted between the *EcoR*I site and the *Spe*I site of the plasmid wherein 16 nucleotides were missing as described above to produce the plasmid pM1081.

(2) Preparation of plasmid pM1253 carrying a nucleotide sequence coding for polypeptide ND38

First, a sense primer 11 (CTGACTAGTGTCGCTAAGGAGCTGAGGAAA) SEQ ID NO: 85 was synthesized. This sense primer 11 contains a nucleotide sequence coding for the signal peptide of the human Fas antigen; a nucleotide sequence coding for the amino acid sequence from lysine (39th amino acid) to lysine (43rd amino acid) in SEQ ID NO: 3; and *Spe*l site (ACTAGT). An antisense primer 11 (TAAGCC-GAAAAACGTCTGAG) SEQ ID NO: 86 was also chemically synthesized on the basis of the nucleotide sequence in the downstream 3' side of the *Apa*l site (GGGCCC) in SEQ ID NO: 15.

A 100 μl solution containing 100 pmol each of the resulting sense primer and the antisense primer; 50 ng of plasmid pEX-hFL1 prepared in Inventive Example 12(1); and 2.5 U of pfu DNA polymerase and 10 μl of pfu buffer attached therewith was prepared. PCR was carried out by repeating the procedure of Inventive Example 18(1), and the PCR product was double digested with *Spel* and *Apal*, and the digestion product was electrophoresed on agarose gel. A DNA fragment of about 400 bp was recovered, and the DNA was purified with QIAEXTM kit. The thus purified DNA fragment of about 400 bp was inserted between the *Spel* site and the *Apal* site of plasmid pM1081 produced in the above (1) to produce plasmid pM1253. (3) Preparation of plasmid pM1254 carrying a nucleotide sequence coding for polypeptide ND40

First, a sense primer 12 (CTGACTAGTGTCGCTCTGAGGAAAGTGGCC) SEQ ID NO: 87 was synthesized. This sense primer contains a nucleotide sequence coding for the signal peptide of the human Fas antigen; a nucleotide sequence coding for the amino acid sequence from leucine (41st amino acid) to alanine (45th amino acid) in SEQ ID NO: 3; and *Spel* site (ACTAGT).

Using the thus synthesized sense primer and antisense primer 11, PCR was carried out by repeating the procedure of the above (2), and the PCR product was inserted into plasmid pM1081 to produce plasmid pM1254.

(4) Preparation of plasmid pM1255 carrying a nucleotide sequence coding for polypeptide ND41

55

First, a sense primer 13 (CTGACTAGTGTCGCTAGGAAAGTGGCCCAT) SEQ ID NO: 88 was synthesized. This sense primer contains a nucleotide sequence coding for the signal peptide of the human Fas antigen; a nucleotide sequence coding for the amino acid sequence from arginine (42nd amino acid) to

hystidine (46th amino acid) in SEQ ID NO: 3; and Spel site (ACTAGT).

Using the thus synthesized sense primer and antisense primer 11, PCR was carried out by repeating the procedure of the above (2), and the PCR product was inserted into plasmid pM1081 to produce plasmid pM1255.

(5) Preparation of plasmid pM1256 carrying a nucleotide sequence coding for polypeptide ND42

First, a sense primer 14 (CTGACTAGTGTCGCTAAAGTGGCCCATTTA) SEQ ID NO: 89 was synthesized. This sense primer contains a nucleotide sequence coding for the signal peptide of the human Fas antigen; a nucleotide sequence coding for the amino acid sequence from lysine (43rd amino acid) to leucine (47th amino acid) in SEQ ID NO: 3; and *Spel* site (ACTAGT).

Using the thus synthesized sense primer and antisense primer 11, PCR was carried out by repeating the procedure of the above (2), and the PCR product was inserted into plasmid pM1081 to produce plasmid pM1256.

(6) Preparation of plasmid pM1257 carrying a nucleotide sequence coding for polypeptide ND43

First, a sense primer 15 (CTGACTAGTGTCGCTGTGGCCCATTTAACA) SEQ ID NO: 90 was synthesized. This sense primer contains a nucleotide sequence coding for the signal peptide of the human Fas antigen; a nucleotide sequence coding for the amino acid sequence from valine (44th amino acid) to threonine (48th amino acid) in SEQ ID NO: 3; and *Spel* site (ACTAGT).

Using the thus synthesized sense primer and antisense primer 11, PCR was carried out by repeating the procedure of the above (2), and the PCR product was inserted into plasmid pM1081 to produce plasmid pM1257.

(7) Preparation of plasmid pM1259 carrying a nucleotide sequence coding for polypeptide CD179

An antisense primer 16 (CTTGGTACCCTATTACTTATATAAGCC) SEQ ID NO: 91 and a sense primer 16 (GAGCTACTGCACTACTGGGC) SEQ ID NO: 92 were synthesized. The antisense primer includes a nucleotide sequence coding for the amino acid sequence from glycine (175th amino acid) to lysine (178th amino acid) in SEQ ID NO: 3; termination codons (TAA, TAG); and *KpnI* site (GGTACC). The sense primer is the sequence located in the upstream 5' side of the *ApaI* site (GGGCCC) in SEQ ID NO: 15, which is the DNA sequence of the extracellular domain of the human Fas ligand.

A 100 µl solution containing 100 pmol of the resulting antisense primer and the sense primer; 50 ng of plasmid pEX-hFL1 prepared in Inventive Example 12(1); and 2.5 U of pfu DNA polymerase and 10 µl of pfu buffer attached therewith was prepared. PCR was carried out by repeating the procedure of Inventive Example 18(1), and the PCR product was double digested with *Apal* and *Kpnl*, and the digestion product was electrophoresed on agarose gel. A DNA fragment of about 170 bp was recovered, and the DNA was purified with QIAEX to the thus purified DNA fragment of about 170 bp was inserted between the *Apal* site and the *Kpnl* site of plasmid pM1250 produced in Inventive Example 18(2). The resulting plasmid was designated pM1259.

(8) Preparation of pM1083, pM1084, pM1085, pM1086, pM1087 and pM1089 for expression in a mamma-

Plasmids pM1253, pM1254, pM1255, pM1256, pM1257 and pM1259 produced in the above (2) to (7) were respectively double digested with *EcoR*I and *Kpn*I, and the digestion products were electrophoresed on agarose gel. A DNA fragment of about 450 bp was recovered in the case of pM1253, pM1254, pM1255, pM1256, and pM1257, and a DNA fragment of about 600 bp was recovered in the case of pM1259. The thus recovered DNAs were purified with QIAEX™ kit. The thus purified DNA fragments of about 450 bp and about 600 bp were respectively inserted between the *EcoR*I site and the *Kpn*I site of plasmid pM1103 used in Inventive Example 18(2) for expression in an animal cell host. The resulting plasmids were designated pM1083 (ND38), pM1084 (ND40), pM1085 (ND41), pM1086 (ND42), pM1087 (ND43), and pM1089 (CD179), respectively.

55

45

15

(9) Introduction into COS cells

pM1070 prepared in Inventive Example 18(2) and pM1083, pM1084, pM1085, pM1086, pM1087, and pM1089 prepared in the above (8) were respectively introduced into COS-1 cells as in the case of Inventive Example 18(3) to produce transformants COS-1/pM1070, COS-1/pM1083, COS-1/pM1084, COS-1/pM1085, COS-1/pM1086, COS-1/pM1087, and COS-1/pM1089 by the procedure as described below.

In 2.5 μI of 10 mM Tris-HCI (pH 7.4)/1 mM EDTA were added 0.5 μg of pM1070, pM1083, pM1084; pM1085, pM1086, pM1087, and pM1089, respectively. To the resulting solutions were added 0.7 ml of D-MEM, (Nissui Pharmaceutical) containing 0.2 mg/ml DEAE-dextran and 50 mM Tris-HCl, pH 8 to prepare DNA-DEAE-dextran mixed solutions. The resulting DNA-DEAE-dextran mixed solutions were respectively added dropwise to a monolayer culture of COS-1 cells in a 6 well plate (9.4 cm²/well, NUNC) that had grown to their semi-confluent stage, and the plate was incubated at 37 °C in the presence of 5% CO₂ to produce the transformants COS-1/pM1070, COS-1/pM1083, COS-1/pM1084, COS-1/pM1085, COS-1/pM1086, COS-1/pM1087, and COS-1/pM1089. After 4 hours of incubation, the DNA-DEAE-dextran mixed solutions were respectively removed, and D-MEM containing 10% FCS (Urban Scientific) was added to the wells. The incubation was continued for another 96 hours, and culture supernatants were respectively collected from the COS-1/pM1070, COS-1/pM1083, COS-1/pM1084, COS-1/pM1085, COS-1/pM1086, COS-1/pM1087, and COS-1/pM1089. The thus collected culture supernatants were used for the following evaluation of their cytotoxic activity. (10) Cytotoxic activity of culture supernatants of the transformants

The cytotoxic activity of the culture supernatants of the transformed COS cells produced in the above (9) was evaluated as in the case of Inventive Examples 8 and 12 by using WC8 cells for the target cells. The evaluation was carried out as described below.

In RPMI1640 medium containing 20 µCi of [51Cr] sodium chromate (NEN) 106 cells of WC8 were incubated at 37 °C for 2 hours to label the WC8 cells with the 51Cr.

The cell culture supernatants produced in the above (9) were respectively added to the reaction solution containing 1 x 10⁴ ⁵¹Cr-labeled cells to a final concentration of 1%, 3%, 10% and 30%, respectively. The cultures were incubated at 37 °C for 4 hours, and cytotoxic activity was evaluated by using the release of ⁵¹Cr for the index.

The results are shown in Fig. 39. As apparent in Fig. 39, the culture supernatants of COS-1/pM1083, COS-1/pM1084, COS-1/pM1085, and COS-1/pM1086 exhibited concentration dependent cytotoxic activity on WC8 cells as in the case of COS-1/pM1070. It was then estimated that the deletion mutants of the human Fas ligand present in such culture supernatants should have an activity of binding with the human Fas antigen to induce the apoptosis. On the other hand, culture supernatants of COS-1/pM1087 and COS-1/pM1089 exhibited a cytotoxic activity on WC8 cells significantly weaker than the supernatant of the COS-1/pM1070, and it was then estimated that the deletion mutants of the human Fas ligand present in such culture supernatants should have a slight or no apoptosis-inducing activity.

Such inactivation is believed to have been caused by the deletion of one or more amino acids on N or C terminus of the Fas ligand that resulted in the alteration of the steric conformation of the Fas ligand. It is then estimated that, when an amino acid sequence capable of restoring the original conformation of the Fas ligand is added on the N or C terminus of the polypeptide having deleted one or more amino acids from its N or C terminus to loose its original conformation, the polypeptide would recover its apoptosis-inducing activity even if the amino acid sequence added were different from the amino acid sequence that had been deleted. Similarly, it is estimated that the once lost apoptosis-inducing activity may be provided with the deletion mutant by introducing in the amino acid sequence of the deletion mutant another mutation that is capable of restoring its original conformation.

(Inventive Example 22) Expression of deletion mutants of the extracellular domain of the human Fas ligand in E. coli.

(1) Preparation of plasmid pM468

Plasmid pM468 is a plasmid derived from plasmid pBR322. Plasmid pM468 has been constructed to include the DNA coding for the function enabling the replication in *E. coli*, ampicillin resistant gene, tryptophan promoter, the signal peptide of alkaline phosphatase (phoA), and human pancreatic trypsin inhibitor. In plasmid pM468, the kanamycin resistant gene of plasmid pM469 (Morishita, H. *et al.*, Thrombosis Research vol. 73, pp 193-204, 1994) is replaced with the ampicillin resistant gene.

(2) Preparation of plasmid pM1059

Plasmid pM468 prepared in the above (1) was double digested with *Hind*III and *BamH*, and the digestion product was separated on 0.8% agarose gel (SeakemGTG, Takara Shuzo Co., Ltd.) to isolate the gel containing the DNA fragment of interest. A DNA fragment of about 3.3 kbp was purified with QIAEX™ kit.

An antisense primer 17 (CGCGGATCCGGTACCTTTTTTGGTAACCGGGGTAAACAG) (SEQ ID NO: 93) and a sense primer 17 (CGCAAGTTCACGTAAAAAGC) (SEQ ID NO: 94) were chemically synthesized. The antisense primer includes *BamH* site (GGATCC), *KpnI* site (GGTACC) and *BstEII* site (GGTTACC), and a sequence coding for the C terminus of the signal peptide of alkaline phosphatase. The sense primer is the sequence located on 5' upstream aside of *HindIII* site in tryptophan promoter. PCR was carried out as described below by using the thus synthesized primers and the plasmid pM 468 as template.

To a 100 μI solution containing the above-described temperate DNA for PCR were added the above-described primers, and PCR was carried out by repeating 30 cycles each comprising 94 °C for 1 minute, 55 °C for 2 minutes, and 72 °C for 3 minutes using Gene AmpTM DNA Amplification Reagent Kit with AmpliTagTM (Takara Shuzo Co., Ltd.).

The resulting PCR product was double digested with *Hind*III and *BamH*I, and the digestion product was electrophoresed on 4% agarose gel to separate a DNA fragment of about 120 bp. The thus separated DNA fragment was purified, and ligated with the above described DNA fragment of about 3.3 kbp from plasmid pM468 using T4DNA ligase (Takara Shuzo Co., Ltd.). *E. coli* JM109 was transformed with the resulting product to produce plasmid pM1059. (3) Preparation of plasmid pM1068 expressing the extracellular domain of the human Fas ligand in the cell of the host E. coli

A sense primer 18 (TTGAAGCTTAAAAAAGGGTATAAAATAAAATGCAGCTCTTCCACCT) SEQ ID NO: 95 and an antisense primer 18 (AAGGTCGACTATTAGAGCTTATATAAGCC) SEQ ID NO: 96 were synthesized in a chemical synthesizer. The sense primer carries a sequence coding for a part of *E. coli* tryptophan promoter/operator, initiation codon (ATG), a sequence coding for the N terminus of the extracellular domain of human Fas ligand of SEQ ID NO: 3, and *Hind*III site (AAGCTT). The antisense primer includes a sequence coding for the C terminus of the extracellular domain of human Fas ligand of sequence ID NO: 3, termination codons (TAA, TAG), and *Sal*I site (GTCGAC).

A 100 μ I solution containing 100 pmol each of the antisense primer and the sense primer; 50 ng of plasmid pBX-hFL1; 20 nmol each of dATP, dCTP, dGTP, and dTTP; and 2.5 units of pfu DNA polymerase and 10 μ I of the pfu buffer attached therewith was prepared, and PCR was carried out by repeating the procedure of Inventive Example 18(1). The resulting PCR product was double digested with *Hind*III and *SaI*I, and the digestion product was electrophoresed on agarose gel. A DNA fragment of about 600 bp was recovered and purified with QIAEXTM kit. The thus purified DNA fragment of about 600 bp was inserted between the *Hind*III site and the *SaI*I site of plasmid pM468 prepared in the above (1) to produce plasmid pM1068.

(4) Preparation of plasmid pM1069 expressing the extracellular domain of the human Fas ligand by secretion from the host E. coli

A sense primer 19 (GGGGGTTACCAAAGCCCAGCTCTTCCACCT) SEQ ID NO: 97 including a sequence coding for a part of the signal peptide of the alkaline phosphatase, a sequence coding for the N terminus of the extracellular domain of human Fas ligand of SEQ ID NO: 3, and *BstEII* site (GGTTACC) was synthesized.

A 100 μI solution containing 100 pmol of the thus synthesized sense primer; 100 pmol of the antisense primer 18 (AAGGTCGACTATTAGAGCTTATATAGCC) which was used in the above (3); 50 ng of plasmid pBX-hFL1; 20 nmol each of dATP, dCTP, dGTP, and dTTP; and 2.5 units of pfu DNA polymerase and 10 μI of pfu buffer attached therewith was prepared, and PCR was carried out by repeating the procedure of Inventive Example 18(1). The resulting PCR product was double digested with *BstE*II and *SaI*I, and the digestion product was electrophoresed on agarose gel. A DNA fragment of about 600 bp was recovered and purified with QIAEX[™] kit. The thus purified DNA fragment of about 600 bp was inserted between the *BstE*II site and the *SaI*I site of plasmid pM1059 prepared in the above (2) to produce plasmid pM1069.

(5) Preparation of plasmid pM1073 expressing the deletion mutant of the extracellular domain of the human Fas ligand (wherein 38 amino acids from the N terminus are deleted) by secretion from the host *E. coli*

A sense primer 20 (CCCGGTTACCAAAGCCAAGGAGCTG) SEQ ID NO: 98 and an antisense primer 20 (TAAGCCGAAAAACGTCTGAG) SEQ ID NO: 99 were chemically synthesized. The sense primer 20 includes a sequence coding for a part of the signal peptide of the alkaline phosphatase; a sequence coding for the N terminus of the extracellular domain of human Fas ligand of SEQ ID NO: 3 from which 38 amino acids from the N terminus are missing; and *BstEII* site (GGTTACC). The antisense primer 20 is the nucleotide sequence in the downstream 3' side of the *ApaI* site (GGGCCC) in SEQ ID NO: 15, which is the DNA sequence coding for the extracellular domain of the human Fas ligand.

A 100 µl solution containing 100 pmol each of the sense primer and the antisense primer; 50 ng of plasmid pBX-hFL1 prepared in Inventive Example 12(1); 20 nmol each of dATP, dCTP, dGTP, and dTTP; and 2.5 units of pfu DNA polymerase and 10 µl of pfu buffer attached therewith was prepared, and PCR was carried out by repeating the procedure of Inventive Example 18(1). The resulting PCR product was double digested with BstEll and Apal, and the digestion product was electrophoresed on agarose gel. A DNA fragment of about 300 bp was recovered and purified with QIAEX™ kit. The thus purified DNA fragment of about 300 bp was inserted between the BstEll site and the Apal site of plasmid pM1069 prepared in the above (4) to produce plasmid pM1073.

(6) Preparation of transformant and expression of human Fas ligand

E. coli JE5505 cell strain was transformed with pM1068, pM1069, and pM1073 prepared in the above (3), (4), and (5), respectively, in accordance with the method described in Hanahan, D., Techniques for Transformation of E. coli, In: DNA Cloning, vol. 1, Glover, D. M. ed., pp. 109-136, IRL Press, 1985, to produce recombinant E. coli JE5505(pM1068), JE5505(pM1069), and JE5505(pM1073).

The resulting transformants were respectively incubated in 5 ml of L broth containing 50 µg/ml ampicillin overnight. 0.5 ml of the culture medium was inoculated in 25 ml of M9CA medium containing 50 µg/ml ampicillin, and the culture was incubated at 37 °C for 3 to 4 hours. When the culture medium exhibited an OD₅₅₀ of approximately 1, 3β-indol acrylic acid (Wako Pure Chemicals) was added to a final concentration of 10 µg/ml, and the culture was incubated for another about 24 hours. The resulting culture mixture was centrifuged to separately recover the supernatant and the cells. (7) Western blotting of the transformant supernatant and cells

Western blotting was carried out by repeating the procedure of Inventive Example 18(5) using a rabbit antiserum capable of recognizing a part of the amino acid sequence of the human Fas ligand (PSPPPEK-KELRKVAH).

To the cells (cells corresponding to 1 ml of the culture medium) of transformants JE5505(pM1068), JE5505(pM1069), and JE5505(pM1073) produced in the above (6) was added 1 ml of RIPA buffer (50 mM Tris-HCI, pH 7.5 containing 150 mM NaCl, 1% NP-40, 0.1% sodium deoxycholate, 0.1% SDS, and 0.2 U/ml Aprotinin), and the mixture was stirred for 30 minutes. The mixture was then centrifuged to recover the supernatant. 10 µl of the thus obtained supernatant from the cells and the supernatant of the culture of the transformant produced in the above (6) were respectively mixed with 5 µl of distilled water. To such mixtures were respectively added a 5 µl solution containing 4% SDS, 80% glycerol, and 0.04% BPB, and a 5 µl solution containing 4% SDS, 80% glycerol, 8% DTT, and 0.04% BPB. The resulting mixtures were respectively incubated at 37 °C for 1 hour, and then, subjected to SDS-polyacrylamide gel electrophoresis. After completing the electrophoresis, the gel was transferred to PVDF membrane (Atto K.K.) at room temperature, at 200 mA for 60 minutes, and the membrane was blocked by the solution of skim milk (Snow Brand Milk Products, Co., Ltd.) at 4 °C overnight. The thus blocked membrane was washed once with PBS, and twice with 0.1% Tween 20/PBS.

The rabbit antiserum as described above was diluted 1,000 times with 0.5% BSA/0.1% Tween 20/PBS, and the membrane was allowed to react with the thus diluted rabbit antiserum at 37 °C for 1 hour. After the completion of the reaction, the membrane was washed twice with 0.1% Tween 20/PBS. The membrane was then immersed in a solution of the peroxidase-labeled anti-rabbit immunoglobulins antibody (Cat. No. P448, DAKO) which had been diluted 500 times with 0.5% BSA/0.1% Tween 20/PBS, and allowed to react at room temperature for 1 hour. The membrane was washed 5 times with 0.1% Tween 20/PBS, and water on the surface was removed. The membrane was then evaluated in ECL system (Amersham).

As shown in Fig. 40, in the case of the cells and the supernatant of JE5505(pM1068), 2 bands corresponding to the extracellular domain of the human Fas ligand were observed about 21 kD and about 23 kD under non-reduced conditions; and one band was found at about 23 kD under reduced conditions.

As shown in Fig. 41, in the case of the cells and the supernatant of JE5505(pM1069), a clear band corresponding to the extracellular domain of the human Fas ligand was observed at about 23 kD both under non-reduced conditions and under reduced conditions.

(Reference Example 1) Cloning of cDNA for Fas ligand derived from gld (C3H gld/gld) mouse

Splenocytes of gld (C3H gld/gld) mouse were cultured in accordance with the procedure described in Inventive Example 14, and synthesis of single-stranded cDNA and PCR were carried out in the same manner as described in Inventive Example 14. The thus obtained PCR product was digested with a restriction enzyme Xbal and isolated using 1% agarose gel to recover a DNA fragment of about 940 bp. This was subcloned into the Xbal site of pBluescript IIKS(+) to determine its nucleotide sequence (SEQ ID NO: 100). When the thus determined nucleotide sequence was compared with the sequence confirmed in Inventive Example 14 (1), it was found that the sequence of the thus obtained PCR product has a mutation in which a T (Thymidine) close to the 3'-end of the sequence confirmed in Inventive Example 14 (1) (position 849 in SEQ ID NO: 32) is mutated into C (Cytosine) (SEQ ID NO: 100). By this mutation of a single base, a mutation occurred also in the amino acid sequence. That is, in the gld mouse, the 273rd amino acid residue in the extracellular domain of the mouse Fas ligand is mutated from phenylalanine to leucine.

(Reference Example 2) Cytotoxic activity of gld mouse-derived Fas ligand

The Xbal fragment of about 940 bp obtained in Reference Example 1 was inserted into the Xbal site of an animal cell expression vector pEF-BOS. COS cells were transformed in the same manner as described in Inventive Example 14 (2). Using the transformed COS cells as effector cells, cytotoxic activity was measured in the same manner as described in Inventive Example 14 (3). As the result, the COS cells transformed with the Fas ligand cDNA obtained from gld mouse did not show the cytotoxic activity (Fig. 26). On the basis of the above results, it was confirmed that normal Fas ligand-induced apoptosis does not occur in the gld mouse which is a model animal of autoimmune diseases.

Based on the results of this time and those reported by Ogasawara J. et al., it was suggested that at least an abnormality in Fas antigen and an abnormality in Fas ligand could be included in the cause of autoimmune diseases. In each case, autoimmune diseases seem to occur because of the lack of ability to induce apoptosis in autoreactive T cells which therefore cannot be removed from the living body.

Thus, it is apparent that there has been provided, in accordance with the present invention, a novel protein which binds to Fas antigen. This novel protein can be developed as therapeutic drugs for the treatment of diseases in which Fas antigen-mediated apoptosis is concerned, such as autoimmune diseases and viral infection. Also, the novel protein can be used as an antigen for the preparation of antibodies and in an assay system in which said protein contained in samples is measured by a competitive reaction using antibodies.

Also, according to the present invention, there is provided a DNA fragment which encodes the novel protein that binds to Fas antigen. This DNA fragment can be used for the industrial production of the above novel protein in a large scale making use of genetic engineering techniques. It can be used also for the preparation of DNA probes. Also, the novel DNA fragment can be used in the gene therapy for the treatment of certain cases of autoimmune diseases in which the mechanism of apoptosis is deleted hereditarily.

In addition, disclosure of the DNA sequence leads to the provision of an oligonucleotide or a derivative thereof which contains a nucleotide sequence complementary to a part of Fas ligand gene or of mRNA for Fas ligand. This oligonucleotide can be used not only for the regulation of the expression of Fas ligand but also as a diagnostic probe.

50

20

```
(2) INFORMATION FOR SEQ ID NO:1:
                SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 137 amino acids
                 (B) TYPE: amino acid
                 (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: protein
            (v) ORIGINAL SOURCE:
                 (A) human
10
                 (C) INDIVIDUAL ISOLATE:
                 (D) DEVELOPMENTAL STAGE: rearrenged
            (vi) IMMEDIATE SOURCE:
                 (B) CLONE: cos/pEx-hFL1
15
            (viii) SEQUENCE DESCRIPTION: SEQ ID NO:1
      Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro
                                             10
                                                                  15
      Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val
20
                        20
                                             25
      Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr
                        35
                                             40-
      Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn
                        50
                                             55
      Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro
25
                        65
                                             70
                                                                  75
      Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr
                        80
                                             85
                                                                  90
      Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe
                        95
                                            100
30
      Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu
                       110
                                            115
      Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr
                       125
      Lys Leu
35
          137
      (2) INFORMATION FOR SEQ ID NO:2:
            (i) SEQUENCE CHARACTERISTICS:
40
                 (A) LENGTH: 138 amino acids
                 (B) TYPE: amino acid
                 (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: protein
            (v) ORIGINAL SOURCE:
45
                 (A) human
                 (C) INDIVIDUAL ISOLATE:
                 (D) DEVELOPMENTAL STAGE: rearrenged
            (vi) IMMEDIATE SOURCE:
                 (B) CLONE: cos/pEx-hFL1
50
            (viii) SEQUENCE DESCRIPTION: SEQ ID NO:2
```

```
Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met
        Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly
                          20
                                               25
                                                                    30
        Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu
                                               40
                          35
        Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn
                          50
                                               55
        Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr
                          65
                                               70
                                                                    75
10
        Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys
                                                                    90
                          80
        Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val
                                              100
                          95
        Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu
15
                         110
                                              115
        Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu
                         125
                                              130
         Tyr Lys Leu
                 138
20
         (2) INFORMATION FOR SEQ ID NO:3:
              (i) SEQUENCE CHARACTERISTICS:
                   (A) LENGTH: 179 amino acids
                   (B) TYPE: amino acid
25
                   (D) TOPOLOGY: linear
              (ii) MOLECULE TYPE: protein
              (v) ORIGINAL SOURCE:
                   (A) human
                   (C) INDIVIDUAL ISOLATE:
30
                   (D) DEVELOPMENTAL STAGE: rearrenged
              (vi) IMMEDIATE SOURCE:
                   (B) CLONE: cos/pEx-hFL1
              (viii) SEQUENCE DESCRIPTION: SEQ ID NO:3
35
        Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu Ser
                                               10
                                                                    15
        Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu Lys Gln Ile Gly
                          20
                                               25
                                                                    .30
        His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala
40
                          35
                                               40
        His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp
                                                                    60
                          50
                                               55
        Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys
                                                                    75
45
        Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
                          80
                                               85
        Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu
                          95
                                              100
                                                                   105
        Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu
                         110
                                              115
                                                                   120
50
```

55

Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln

```
Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr
                        140
                                             145
                                                                  150
5
        Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val
                                             160
                        155
        Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
                                             175
                                                              179
                        170
        (2) INFORMATION FOR SEQ ID NO:4:
10
                  SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 281 amino acids
                  (B) TYPE: amino acid
                  (D) TOPOLOGY: linear
15
             (ii) MOLECULE TYPE: protein
             (v) ORIGINAL SOURCE:
                  (A) human
                  (D) T lymphocyte
20
             (viii) SEQUENCE DESCRIPTION: SEQ ID NO:4
        Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val
25
        Asp Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu
                         20
        Pro Cys Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro
                         35
                                              40
                                                                   45
        Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro
                                              55
                                                                   60
30
        Pro Pro Leu Pro Pro Leu Pro Pro Leu Lys Lys Arg Gly
                                              70
                         65
        Asn His Ser Thr Gly Leu Cys Leu Leu Val Met Phe Phe Met Val
                                              85
                         80
        Leu Val Ala Leu Val Gly Leu Gly Leu Gly Met Phe Gln Leu Phe
35
                                             100
                                                                  105
                          95
        His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu Ser Thr Ser Gln
                                             115
                        110
       Met His Thr Ala Ser Ser Leu Glu Lys Gln Ile Gly His Pro Ser
                                             130
                                                                  135
                        125
        Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr
                        140
                                             145
                                                                  150
        Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr
                        155 -
                                             160
        Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly
                        170
                                             175
                                                                  180
45
        Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val
                                                                  195
                                             190
                        185
        Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys
                        200
                                             205
                                                                  210
        Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met Met
                                                                  225
                                             220
                        215
50
        Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
                                             235
                        230
```

245

260

Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp

His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu

250

265

255

270

Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu 280 281 275 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: 10 (A) LENGTH: 137 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (v) ORIGINAL SOURCE: rat 15 (viii) SEQUENCE DESCRIPTION: SEQ ID NO:5 Ser Val Ala His Leu Thr Gly Asn Pro Arg Ser Arg Ser Ile Pro 20 Leu Glu Trp Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Ala Gly Leu Tyr 40 Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Ser 50 55 Gln Pro Leu Ser His Lys Val Tyr Met Arg Asn Phe Lys Tyr Pro 65 Gly Asp Leu Val Leu Met Glu Glu Lys Lys Leu Asn Tyr Cys Thr 80 85 Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val Phe 30 95 100 Asn Leu Thr Val Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu 115 110 Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu Tyr 135 125 130 35 Lys Leu 137 (2) INFORMATION FOR SEQ ID NO:6: (i) SEQUENCE CHARACTERISTICS: 40 (A) LENGTH: 138 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (v) ORIGINAL SOURCE: rat (viii) SEQUENCE DESCRIPTION: SEQ ID NO:6 Arg Ser Val Ala His Leu Thr Gly Asn Pro Arg Ser Arg Ser Ile 50

54

```
Pro Leu Glu Trp Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly
                          20
                                               25
                                                                    30
        Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Ala Gly Leu
5
                          35
                                               40
        Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn
                          50
                                              55
        Ser Gln Pro Leu Ser His Lys Val Tyr Met Arg Asn Phe Lys Tyr
                          65
                                              70
        Pro Gly Asp Leu Val Leu Met Glu Glu Lys Lys Leu Asn Tyr Cys
10
                          80
                                              85
                                                                    90
        Thr Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val
                          95
                                             100
        Phe Asn Leu Thr Val Ala Asp His Leu Tyr Val Asn Ile Ser Gln
                         110
                                             115
                                                                  120
15
        Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu
                         125
                                             130
                                                                  135
        Tyr Lys Leu
                138
```

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 179 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(v) ORIGINAL SOURCE: rat

(viii) SEQUENCE DESCRIPTION: SEQ ID NO:7

```
30
        Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu Phe
                                              10
        Thr Asn His Ser Leu Arg Val Ser Ser Phe Glu Lys Gln Ile Ala
                         20
                                              25
        Asn Pro Ser Thr Pro Ser Glu Thr Lys Lys Pro Arg Ser Val Ala
                         35
                                              40
                                                                   45
35
        His Leu Thr Gly Asn Pro Arg Ser Arg Ser Ile Pro Leu Glu Trp
                         50
                                              55
        Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys
                         65
                                              70
                                                                   75
        Lys Gly Gly Leu Val Ile Asn Glu Ala Gly Leu Tyr Phe Val Tyr
                         80
                                              85
                                                                   90
        Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Ser Gln Pro Leu
                         95
                                             100
                                                                  105
        Ser His Lys Val Tyr Met Arg Asn Phe Lys Tyr Pro Gly Asp Leu
                        110
                                             115
                                                                  120
        Val Leu Met Glu Glu Lys Lys Leu Asn Tyr Cys Thr Thr Gly Gln
45
                        125
                                             130
                                                                  135
        Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr
                        140
                                             145
        Val Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile
                        150
                                             155
50
        Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu Tyr Lys Leu
                        165
                                             170
                                                             179
```

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 amino acids
 - (B) TYPE: amino acid
- (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein
- (v) ORIGINAL SOURCE: rat
- (viii) SEQUENCE DESCRIPTION: SEQ ID NO:8

	Met	Gln	Gln	Pro	Val	Asn	Tyr	Pro	Cys	Pro 10	Gln	Ile	Tyr	Trp	Val
15	Asp	Ser	Ser	Ala	Thr 20	Ser	Pro	Trp	Ala		Pro	Gly	Ser	Val	
	Ser	Суз	Pro	Ser	Ser 35	Gly	Pro	Arg	Gly	Pro 40	Gly	Gln	Arg	Arg	Pro 45
					50					55			Pro		6.0
20					65					70			Lys		75
				•	80					85			Leu		90
			•		95		•		-	100			His		105
25			•		110		_			115			Ser		120
					125	_				130			Thr		135
30			•	•	140	-				145			Gly		150
	_		-		155				-	160	-		Tyr	•	165
					170		_	_	-	175	_	_	Leu		180
35				•	185	•			-	190	•		Tyr		195
, .					200					205			Val	-	210
	-			•	215		-	•		220	•		Glu		225
40		,		_	230			_		235	_		His		240
					245					250		•	His		255
4E					260				TIE	265	rne	GIU	Glu	ser	Lys 270
45	Inr	rne	Phe	сту	275	Tyr	rās	278							

- (2) INFORMATION FOR SEQ ID NO:9:
- 50 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 137 amino acids

```
(B) TYPE: amino acid
                   (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: protein
5
             (v) ORIGINAL SOURCE: mouse
             (viii) SEQUENCE DESCRIPTION: SEQ ID NO:9
        Ser Val Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro
10
        Leu Glu Trp Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val
                          20
                                              25
        Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr
        Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn
15
                                              55
                          50
        Gln Pro Leu Asn His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro
                                              70
                          65
        Glu Asp Leu Val Leu Met Glu Glu Lys Arg Leu Asn Tyr Cys Thr
                          80
                                              85
        Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val Phe
20
                          95
                                             100
        Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu
                                             115
                         110
        Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu Tyr
                         125
                                             130
25
        Lys Leu
             137
         (2) INFORMATION FOR SEQ ID NO:10:
              (i) SEQUENCE CHARACTERISTICS:
30
                   (A) LENGTH: 138 amino acids
                   (B) TYPE: amino acid
                   (D) TOPOLOGY: linear
              (ii) MOLECULE TYPE: protein
35
              (v) ORIGINAL SOURCE: mouse
              (viii) SEQUENCE DESCRIPTION: SEQ ID NO:10
        Arg Ser Val Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile
40
                                              10
        Pro Leu Glu Trp Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly
                          20
                                              25
        Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu
                          35
45
         Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn
                                               55
                          50
        Asn Gln Pro Leu Asn His Lys Val Tyr Met Arg Asn Ser Lys Tyr
                                              70
                          65
        Pro Glu Asp Leu Val Leu Met Glu Glu Lys Arg Leu Asn Tyr
                                                                  Cys
```

55

50

Thr Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val

```
95
                                            100
       Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Ile Ser Gln
                        110
                                            115
                                                                 120
       Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu
                        125
                                            130
                                                                 135
       Tyr Lys Leu
               138
       (2) INFORMATION FOR SEQ ID NO:11:
10
             (i) SEQUENCE CHARACTERISTICS:
                  (A) LENGTH: 179 amino acids
                  (B) TYPE: amino acid
                  (D) TOPOLOGY: linear
15
             (ii) MOLECULE TYPE: protein
             (v) ORIGINAL SOURCE: mouse
             (viii) SEQUENCE DESCRIPTION: SEQ ID NO:11
20
       Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu Phe
         1
       Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys Gln Ile Ala
                                             25
       Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser Val Ala
25
                         35
       His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp
                         50
                                             55
                                                                  60
       Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys
                         65
                                             70
       Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
30
                         80
                                             85
       Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu
                         95
                                            100
       Asn His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu
                                            115
                       110
                                                                 120
35
       Val Leu Met Glu Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln
                        125
                                            130
       Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr
                       140
                                            145
       Ser Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile
40
                        155
                                            160
       Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu Tyr Lys Leu
                       170
                                            175
                                                             179
       (2) INFORMATION FOR SEQ ID NO:12:
             (i) SEQUENCE CHARACTERISTICS:
                     LENGTH: 279 amino acids
                  (A)
                  (B)
                      TYPE: amino acid
                      TOPOLOGY: linear
                  (D)
            (ii) MOLECULE TYPE: protein
50
            (v) ORIGINAL SOURCE: mouse
```

58

(viii) SEQUENCE DESCRIPTION: SEQ ID NO:12 Met Gln Gln Pro Met Asn Tyr Pro Cys Pro Gln Ile Phe Trp Val

1.5 Asp Ser Ser Ala Thr Ser Ser Trp Ala Pro Pro Gly Ser Val Phe Pro Cys Pro Ser Cys Gly Pro Arg Gly Pro Asp Gln Arg Arg Pro Pro Pro Pro Pro Pro Val Ser Pro Leu Pro Pro Pro Ser Gln Pro Leu Pro Leu Pro Pro Leu Thr Pro Leu Lys Lys Asp His Asn Thr Asn Leu Trp Leu Pro Val Val Phe Phe Met Val Leu Val Ala Leu Val Gly Met Gly Leu Gly Met Tyr Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys Gln Ile Ala Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser Val Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp Glu Asp Thr Tyr Gly 1 65 Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met Glu Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser

Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser

Lys Thr Phe Phe Gly Leu Tyr Lys Leu

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 411 bases
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

- (v) ORIGINAL SOURCE:
 - (A) human

(viii) SEQUENCE DESCRIPTION: SEQ ID NO:13

	AAA	GTG	GCC	CAT	TTA	ACA	GGC	AAG	TCC	AAC	TCA	AGG	TCC	ATG	CCT	45
5	CTG	GAA	TGG	GAA	GAC	ACC	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	GTG	90
	AAG	TAT	AAG	AAG	GGT	GGC	CTT	GTG	ATC	AAT	GAA	ACT	GGG	CTG	TAC	135
	TTT	GTA	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT.	CAA	TCT	TGC	AAC	AAC	180
10	CTG	ccc	CTG	AGC	CAÇ	AAG	GTC	TAC	ATG	AĞG	AAC	TCT	AAG	TAT	ccc	225
	CAG	GAT	CTG	GTG	ATG	ATG	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	ACT	270
	ACT	GGG	CAG	ATG	TGG	GCC	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	TTC	315
15	AAT	CTT	ACC	AGT	GCT	GAT	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	CTC	360
	TCT	CTG	GTC	AAT	TTT	GAG	GAA	тст	CAG	ACG	TTT	TTC	GGC	TTA	TAT	405
20	AAG	CTC														411
	(2)	INF	ORMA:	rion	FOR	SEQ	ID 1	NO:1	4:							
25 30		(i:	() () () (i) M(A) LI B) T: C) S: O) T(OLECT	CE CI ENGTI YPE: TRANI OPOLO ULE T	H: 4: nuc: DEDNI DGY: TYPE	l4 ba leic ESS: line : DN	ases acio sino ear	i i							
30		(- /		A) hu		JUNC:	.							,		
		(v	iii)	SEQ	JENCI	E DES	SCRI	PTION	N: SE	EQ II	ON C	:14	•			
35	AGG	AAA	GTG	GCC	CAT	TTA	ACA	GGC	AAG	TCC	AAC	TCA	AGG	TCC	ATG	45
	CCT	CTG	GAA	TGG	GAA	GAC	ACC	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	90
	GTG	AAG	TAT	AAG	AAG	GGT	GGC	CTT	GTG	ATC	AAT	GAA	ÄCT	GGG	CTG	135
40	TAC	TTT	GTA	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAA	TCT	TGC	AAC	180
	AAC	CTG	ccc	CTG	AGC	CAC	AAG	GTC	TAC	ATG	AGG	AAC	TCT	AAG	TAT	225
15 ·	ccc	CAG	GAT	CTG	GTG	ATG	ATG	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	270
45	ACT	ACT	GGG	CAG	ATG	TGG	GCC	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	315
	TTC	AAT	CTT	ACC	AGT	GCT	GAT	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	360
50	CTC	TCT	CTG	GTC	AAT	TTT	GAG	GAA	TCT	CAG	ACG	TTT	TTC	GGC	TTA	405
	TAT	AAG	CTC									•				414

	(2)	INFO	RMAT	CION	FOR	SEQ	ID N	10:15	i :							
5		(i)	(<i>I</i> (E	QUENCA) LE B) TY C) ST	NGTE PE: RANI	i: 53 nucl	37 ba Leic ESS:	ses acio sino	i							
10		(i:	L) MO	DLECU	JLE 1	YPE:	DN?	4							٠	
		(v)		IGINA A) hu		OURCE	Ξ:									
15		(v:	iii)	SEQU	JENCE	E DES	CRIE	PTION	1: SE	EQ II	ОИ	:15				
	CAG	CTC	TTC	CAC	CTA	CAG	AAG	GAG	CTG	GCA	GAA	CTC	CGA	GAG	TCT	45
	ACC	AGC	CAG	ATG	CAC	ACA	GCA	TCA	TCT	TTG	GAG	AAG	CAA	ATA	GGC	90
20	CAC	ccc	AGT	CCA	ccc	CCT	GAA	AAA	AAG	GAG	CTG	AGG	AAA	GTG	GCC	13
	CAT	TTA	ACA	GGC	AAG	TCC	AAC	TCA	AGG	TCC	ATG	CCT	CTG	GAA	TGG	18
	GAA	GAC	ACC	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	GTG	AAG	TÀT	AAG	22
25	AAG	GGT	GGC	CTT	GTG	ATC	AAT	GAA	ACT	GGG	CTG	TAC	TTT	GTA	TAT	27
	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAA	TCT	TGC	AAC	AAC	CTG	ccc	CTG	31
	AGC	CAC	AAG	GTC	TAC	ATG	AGG	AAC	TCT	AAG	TAT	ccc	CAG	GAT	CTG	36
30	GTG	ATG	ATG	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	ACT	ACT	GGG	CAG	40
	ATG	TGG	GCC	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	TTC	AAT	CTT	ACC	45
35	AGT	GCT	GAT	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	CTC	TCT	CTG	GTC	49
	AAT	TTT	GAG	GAA	TÇT	CAG	ACG	TTT	TTC	GGC	TTA	TAT	AAG	CTC		53
	(2)	INF	ORMA!	TION	FOR	SEQ	ID 1	NO:1	6:							
40		(i	-	QUENC A) Li					CS:							
			Ò	B) T:	YPE:	nuc.	leic	acio								
		(i.	(1	D) TO	OPOL	OGY:	line	ear						•		
45				IGIN			_		•							
		•	(I	A) hi	namı										-	
50		-	((C) CI	LONE	: pB	X-hF	L1 PTIO	N: SI	EQ II	ON C	:16	•			
		•														

ATG CAG CAG CCC TTC AAT TAC CCA TAT CCC CAG ATC TAC TGG GTG . 45

	GAC	AGC	AGT	GCC	AGC	TCT	ccc	TGG	GCC	CCT	CCA	GGC	ACA	GTT	CTT	90
	ccc	TGT	CCA	ACC	TCT	GTG	ccc	AGA	AGG	CCT	GGT	CAA	AGG	AGG	CCA	135
5	CCA	CCA	CCA	CCG	CCA	CCG	CCA	CCA	CTA	CCA	CCT	CCG	CCG	CCG	CCG	180
	CCA	CCA	CTG	CCT	CCA	CTA	CCG	CTG	CCA	ccc	CTG	AAG	AAG	AGA	GGG	225
10	AAC	CAC	AGC	ACA	GGC	CTG	TGT	CŢC	CTT	GTG	ATG	TTT	TTC	ATG	GTT	270
	CTG	GTT	GCC	TTG	GTA	GGA	TTG	GGC	CTG	GGG	ATG	TTT	CAG	CTC	TTC	315
	CAC	CTA	CAG	AAG	GAG	CTG	GCA	GAA	CTC	CGA	GAG	TCT	ACC	AGC	CAG	360
15	ATG	CAC	ACA	GCA	TCA	TCT	TTG	GAG	AAG	CAA	ATA	GGC	CAC	ccc	AGT	405
	CCA	ccc	CCT	GAA	AAA	AAG	GAG	CTG	AGG	AAA	GTG	GCC	CAT	TTA	AÇA	450
	GGC	AAG	TCC	AAC	TCA	AGG	TCC	ATG	CCT	CTG	GAA	TGG	GAA	GAC	ACC	495
20	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	GTG	AAG	TAT	AAG	AAG	GGT	GGC	540
	CTT	GTG	ATC	AAT	GAA	ACT	GGG	CTG	TAC	TTT	GTA	TAT	TCC	AÁA	GTA	585
25	TAC	TTC	CGG	GGT	CAA	TCT	TGC	AAC	AAC	CTG	ccc	CTG	AGC	CAC	AAG	630
	GTC	TAC	ATG	AGG	AAC	TCT	AAG	TAT	ссс	CAG	GAT	CTG	GTG	ATG	ATG	675
	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	ACT	ACT	GGG	CAG	ATG	TGG	GCC	720
30	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	TTC	AAT	CTT	ACC	AGT	GCT	GAT	765
	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	СТС	TCT	CTG	GTC	AAT	TTT	GAG	810
	GAA	TCT	CAG	ACG	TTT	TTC	GGC	TTA	TAT	AAG	CTC					843
35	(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	NO:17	7:							•
40		(i) (ii	(E (C (D) SI	NGTH PE: RANE	i: 41 nucl EDNE GY:	l ba eic SS: line	ses acio sino ar	i jle	IA						
4 5		(vi	A) I (. C)	GINA hu MMED C SEQU	man IATE LONE	SOU	IRCE :	15	I: SĒ	Q ID	NO:	17				
50	AGT	GTG	GCC	CAC	TTA	ACA	GGG	AAC	ссс	CGC	TCA	AGG	TCC	ATC	CCT	45
	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	ACT	GCT	TTG	ATC	TCT	GGA	GTG	90

	AAG	TAT	AAG	AAA	GGC	GGC	CTT	GTG	ATC	AAT	GAG	GCT	GGG	TTG	TAC	135
_	TTC	GTA	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AGC	180
5	CAG	ccc	CTA	AGC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TTT	AAG	TAT	CCT	225
	GGG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	AAG	TTG	AAT	TAC	TGC	ACT	270
10	ACT	GGC	CAG	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTA	GGG	GCA	GTA	TTT	315
	AAT	CTT	ACC	GTT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	CTC	360
	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTT	GGC	TTA	TAT	405
15	AAG	CTT													•	411
	(2)	INF	ORMA	rion	FOR	SEQ	ID I	NO:18	8:							
20			(E	A) LE B) T' C) S' C) T(ENGTI (PE : [RANI OPOL(H: 4: nuc: DEDNI DGY:	l4 ba leic ESS: line	ases acio sino ear	d gle	ΔV						
25		(v)	ORI (2	IGINA A) ra	AL SO At IATE	OURCE	E: RCE:		, mrt	.			-			
30		(v:	lii)						N: SE	EQ II	ON C	:18				
	AGG	AGT	GTG	GCC	CAC	TTA	ACA	GGG	AAC	ccc	CGC	TCA	AGG	TCC	ATC	45
	CCT	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GĞA	ACT	GCT	TTG	ATC	TCT	GGA	90
35	GTG	AAG	TAT	AAG	AAA	GGC	GGC	CTT	GTG	ATC	AAT	GAG	GCT	GGG	TTG	(135
	TAC	TTC	GTA	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	180
	AGC	CAG	ccc	CTA	AGC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TTT	AAG	TAT	225
10	CCT	GGG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	AAG	TTG	AAT	TAC	TGC	270
	ACT	ACT	GGC	CAG	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTA	GGG	GCA	GTA	315
4 5	TTT	AAT	CTT	ACC	GTT	GCT	GAC	CAT	TTA	TAT	GTC	AÁC	ATA	TCT	CAA	360
	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTT	GGC	TTA	405
	TAT	AAG	CTT													414
io	(2)	INFC	RMAT	NOI	FOR	SEQ	ID N	0:19):							
		123	CEO		E 011	2020	mrn r		· c .							

5		(i :	() () ()	A) L: 3) T: C) S: O) T(OLEC!	YPE : TRANI OPOLO	nuc: DEDNI DGY:	leic ESS: line	acio sino ear	gle	NA.						
10		(V:	() (I i) II ()	IGINA A) ra B) SI MMEDI C) CI SEQU	at TRAII IATE LONE	N: P(SOUI : pTi	C60-6 RCE:	15		EQ II	O NO	:19				
	CAA	CTC	TTT	CAT	CTA	ĊAG	AAG	GAA	CTG	GCA	GAA	CTC	CGT	GAG	TTC	45
15	ACC	AAC	CAC	AGC	CTT	AGA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	ATA	GCC	90
	AAC	CCC	AGC	ACA	ccc	TCT	GAA	ACC	AAA	AAG	CCA	AGG	AGT	GTG	GCC	135
20	CAC	TTA	ACA	GGG	AAC	ccc	CGC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	180
	GAA	GAC	ACA	TAT	GGA	ACT	GCT	TTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	225
	AAA	GGC	GGC	CTT	GTG	ATC	AAT	GAG	GCT	GGG	TTG	TAC	TTC	GTA	TAT	270
25	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AGC	CAG	ccc	CTA	315
	AGC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TTT	AAG	ŤAT	CCT	GGG	GAT	CTG	360
	GTG	CTA	ATG	GAG	GAG	AAG	AAG	ŢTG	AAT	TAC	TGC	ACT	ACT	GGC	CAG	405
30	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTA	GGG	GCA	GTA	TTT	AAT	CTT	ACC	450
	GTT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	495
35	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTT	GGC	TTA	TAT	AAG	CTT		537
	(2)	INFO	ORMAT	CION	FOR	SEQ	ID N	10:20) :							
1 0			(Z (E (C	QUENC A) LE B) TY C) ST O) TO OLECU	NGTH PE: RAND	H: 83 nucl EDNE GY:	eic SS:	ases acio sino near	i gle	IA.						•
45		•	(<i>P</i> (E .) IM	GINA A) ra B) SI IMEDI C) CI	t RAIN ATE	I: PC	:60-c		-2					•		
5 <i>0</i>		(vi		SEQU		-			I: SE	O ID	NO:	20				
- •	ATG			CCC									TAC	TGG	GTÀ	45
	-															

	GAC	AGC	AGT	GCC	ACT	TCT	CCT	TGG	GCT	CCT	CCA	GGG	TCA	GTT	TTT	90
	TCT	TGT	CCA	TCC	TCT	GGG	CCT	AGA	ĠGG	CCA	GGA	CAA	. AGG	AGA	CCA	135
5	CCG	CCT	CCA	CCA	CCA	CCT	CCA	TCA	CCA	CTA	CCA	CCG	CCT	TCC	CAA	180
	CCA	ccc	CCG	CTG	CCT	CCA	CTA	AGC	CCT	CTA	AAG	AAG	AAG	GAC	AAC	225
10	ATA	GAG	CTG	TGG	CTA	CCG	GTG	ATA	TTT	TTC	ATG	GTG	CTG	GTG	GCT	270
70	CTG	GTT	GGA	ATG	GGG	TTA	GGA	ATG	TAT	CAA	CTC	TTT	CAT	CTA	CAG	315
	AAG	GAA	CTG	GCA	GAA	CTC	CGT	GAG	TTC	ACC	AAC	CAC	AGC	CTT	AGA	360
15	GTA	TCA	TCT	TTT	GAA	AAG	CAA	ATA	GCC	AAC	ccc	AGC	ACA.	CCC	TCT	405
	GAA	ACC	AAA	AAG	CCA	AGG	AGT	GTG	GCC	CAC	TTA	ACA	GGG	AAC	CCC	450
	CGC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	ŢĢĢ	GAA	GAC	ACA	TAT	GGA	ACT	495
20	GCT	TTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	AAA	GGC	GGC	CTT	GTG	ATC	540
	AAT	GAG	GCT	GGG	TTG	TAC	TTC	GTA	TAT	TCC	AAA	GTA	TAC	TTC	CGG	585
25	GGT	CAG	TCT	TGC	AAC	AGC	CAG	ccc	CTA	AGC	CAC	AAG	GTC	TAT	ATG	630
	AGG	AAC	TTT	AAG	TAT	CCT	GGG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	675
	AAG	TTG	AAT	TAC	TGC	ACT	ACT	GGC	CAG	ATA	TGG	GCC	CAC	AGC	AGC	720
30	TAC	CTA	GGG	GCA	GTA	TTT	AAT	CTT	ACC	GTT	GCT	GAC	CAT	TTA	TAT	765
	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	810
	ACC	TTT	TTT	GGC	TTA	TAT	AAG	CTT								834
35		T175														

- (2) INFORMATION FOR SEQ ID NO:21:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 411 bases
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ii) MOLECULE TYPE: cDNA to mRNA
 - (v) ORIGINAL SOURCE:
 - (A) mouse
 - (vi) IMMEDIATE SOURCE:
 - (C) CLONE: pBL-MFLW4
- (viii) SEQUENCE DESCRIPTION: SEQ ID NO:21
- AGT GTG GCC CAT TTA ACA GGG AAC CCC CAC TCA AGG TCC ATC CCT

55

	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	ACC	GCT	CTG	ATC	TCT	GGA	GTG	90
	AAG	TAT	AĄG	AAA	GGT	GGC	CTT	GTG	ATC	AAC	GAA	ACT	GGG	TTG	TAC	135
5	TTC	GTG	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AAC	180
	CAG	CCC	CTA	AAC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TCT	AAG	TAT	CCT	225
10	GAG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	AGG	TTG	AAC	TAC	TGC	ACT	270
	ACT	GGA	CAG	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTG	GGG	GCA	GTA	TTC	315
	AAT	CTT	ACC	AGT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	CTC	360
15	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTC	GGC	TTG	TAT	405
	AAG	CTT													•	411
	(2)	INF	ORMA'	TION	FOR	SEQ	ID I	NO:2	2:	•						
20		(i)) SE	QUEN	CE C	HARA	CTER	ISTI	cs:				4	•		
			()	A) LI B) Ti	YPE:	nuc.	leic	aci								
				C) S: D) T(gle							
25		(i:	i) M	OLEC	JLE !	TYPE	: cDi	NA to	o mRI	NA						
		(v)		IGINA A) ma		DURC	€:									
30		(V:		MMED:				LW4								
		(v:	iii)	SEQ	JENC	E DES	SCRI	PTIO	N: SI	EQ II	ON O	: 22				
	AGG	AGT	GTG	GCC	CAT	TTA	ACA	GGG	AAC	CCC	CAC	TCA	AGG	TCC	ATC	45
35	CCT	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	ACC	GCT	CTG	ATC	TCT	GGA	90
•	GTG	AAG	.TAT	AAG	AAA	GGT	GGC	CTT	GTG	ATC	AAC	GAA	ACT	GGG	TTG	135
	TAC	TTC	GTG	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	180
40	AAÇ	CAG	ccc	CTA	AAC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TCT	AAG	TAT	225
	CCT	GAG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	AGG	TTG	AAC	TAC	TGC	270
46	ACT	ACT	GGA	CAG	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTG	GGG	GCA	GTA	315
45	TTC	AAT	CTT	ACC	AGT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	360
	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTC	GGC	TTG	405
50	TAT	AAG	CTT													414
	(2)	INFO	RMAT	пои	FOR	SEQ	ID N	10:23	3:							

5		(i:	(2 (1 (0	A) L1 B) T1 C) S1 O) T0	ENGTI YPE: TRANI DPOLO	nuc. DEDNI	37 ba leic ESS: line	ases acio sino ear	d gle	NA	-					
10		•	i) II	A) mo	ouse	SOUI	RCE:	LW4								
		(v:	iii)	SEQ	JENC	E DES	SCRI	OITS	N: SI	EQ II	ои с	:23				
15	CAG	CTC	TTC	CAC	CTG	CAG	AAG	GAA	CTG	GCA	GAA	CTC	CGT	GAG	TTC	45
	ACC	AAC	CAA	AGC	CTT	AAA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	ATA	GCC	90
	AAC	ccc	AGT	ACA	ccc	TCT	GAÄ	AAA	AAA	GAG	CCG	AGG	AGT	GTG	GCC	135
20	CAT	TTA	ACA	GGG	AAC	ccc	CAC	TCA	AGG	TCC	ATC	ССТ	CTG	GAA	TGG	180
	GAA	GAC	ACA	TAT	GGA	ACC	GCT	CTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	225
25	AAA	GGT	GGC	CTT	GTG	ATC	AAC	GAA	ACT	GGG	TTG	TAC	TTC	GTG	TAT	270
- -	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AAC	CAG	ccc	CTA	315
	AAC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TCT	AAG	TAT	CCT	GAG	GAT	CTG	360
30	GTG	CTA	ATG	GAG	GAG	AAG	AGG	TTG	AAC	TAC	TGC	ACT	ACT	GGA	CAG	405
	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTG	GGG	GCA	GTA	TTC	AAT	CTT	ACC	450
*	AGT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	495
35	AAT	TTT	GAG	GAA	TCT	AAG,	ACC	TTT	TTC	GGC	TTG	TAT	AAG	СТТ		537
	(2)	INF	ORMA!	FION	FOR	SEQ	ID 1	NO : 24	4:							
40		(i)	(E	A) Li B) Ti	CE CI ENGTI (PE: TRANI	i: 83	37 ba Leic	ases acid	i					·		
		(i:	I) L) MC		OPOLO				mRi	۱A						
4 5			L) IN	A) mo AMEDI	ouse	SOUF	RCE:									
50 .		(vi	Lii)						1: SE	EQ 10	NO:	24		•		
	ATG	CAG	CAG	CCC	ATG	AAT	TAC	CCA	TGT	CCC	CAG	ATC	TTC	TGG	GTA	45

	GAC	AGC	AGT	GCC	ACT	TCA	TCT	TGG	GCT	CCT	CCA	GGG	TCA	GTT	TTT	90	
	ccc	TGT	CCA	TCT	TGT	GGG	CCT	AGA	GGG	CCG	GAC	CAA	AGG	AGA	CCG	135	
5.	CCA	CCT	CCA	CCA	CCA	ССТ	GTG	TCA	CCA	CTA	CCA	CCG	CCA	TCA	CAA	180	
	CCA	CTC	CCA	CTG	CCG	CCA	CTG	ACC	ССТ	CTA	AAG	AAG	AAG	GAC	CAC	225	
	AAC	ACA	AAT	CTG	TGG	CTA	CCG	GTG	GTA	TTT	TTC	ATG	GTT	CTG	GTG	270	
10	GCT	CTG	GTT.	GGA	ATG	GGA	TTA	GGA	ATG	TAT	CAG	CTC	TTC	CAC	CTG	315	
	CAG	AAG	GAA	CTG	GCA	GAA	CTC	CGT	GAG	TTC	ACC	AAC	CAA	AGC	CTT	360	
15	AAA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	ATA	GCC	AAC	ccc	AGT	ACA	ССС	405	
	TCT	GAA	AAA	AAA	GAG	CCG	AGG	AGT	GTG	GCC	CAT	TTA	ACA	GGG	AAC	450	
	CCC	CAC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	495	
20	ACC	GÇT	CTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	AAA	GGT	GGC	CTT	GTG	540	
	ATC	AAC	GAA	ACT	GGG	TTG	TAC	TTC	GTG	TAT	TCC	AAA	GTA	TAC	TTC	585	
	CGG	GGT	CAG	TCT	TGC	AAC	AAC	CAG	ccc	CTA	AAC	CAC	AAG	GTC	TAT	630	•
25	ATG	AGG	AAC	TCT	AAG	TAT	CCT	GAG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	675	
	AAG	AGG	TTG	AAC	TAC	TGC	ACT	ACT	GGA	CAG	ATA	TGG	GCC	CAC	AGC	720	
	AGC	TAC	CTG	GGG	GCA	GTA	TTC	AAT	CTT	ACC	AGT	GCT	GAC	CAT	TTA	765	
30	TAT	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	810	
	AAG	ACC	TTT	TTC	GGC	TTG	TAT	AAG	CTT							837	
	(2)	INFO	RMAT	ON	FOR	SEQ	ID N	10:25	:								
35		(i)	(A (B (C	L) LE () TX () ST	E CH INGTH IPE: IRAND IPOLO	: 16 amin EDNE	23 a o ac SS:	mino id sing	aci	ds							
40		(iv) MC) FE (D	LECU ATUR	LE T	YPE: INFO	CDN RMAT	A to			-3						
45			(A (B) ra		: PC	60-d	.105-	2								
			(B) CL	ONE :			TION	: SE	Q ID	NO:	25					
50	GTCC	TTGA	CA C	TTCA	GTCT	C CA	CAAG	ACTG	AGA	GGAG	GAA	ACCC	TTTC			GTCCT TGGGT	10 70

	GCC						AAT										118
		Met	Gln	Gln	Pro	Val	Asn	Tyr	Pro	Cys		Gln	Ile	Tyr	Trp		
	CAC	J C C	N C TT	ccc	a CT	ייים ייי	ССТ	TICC	COM	CCT	10	ccc	mc z	C THE		15 mcm	100
5 _	Aen	Ser	Ser	Ala	Thr	Ser	Pro	Trn	Δla	Pro	Pro	GGG Glv	Ser	Val	Dhe	TCT Ser	166
	1101	001			20	001		1	1110	25		011	JCI	VU.1	30	Ser	
	TGT	CCA	TCC	TCT	GGG	CCT	AGA	GGG	CCA	GGA	CAA	AGG	AGA	CCA		CCT	214
							Arg										
				35					40					45			
10							CCA										262
	Pro	Pro		Pro	Pro	Ser	Pro		Pro	Pro	Pro	Ser		Pro	Pro	Pro	
	СТС	ССТ	50 CCA	СТА	ACC	ССТ	CTA	55	220	AAC	GAC	3 3 C	60 גידא	GNG	CTC	TCC	310
							Leu										310
		65					70	-,-	-1-	-10		75		0			
15							ATG										358
			Val	Ile	Phe		Met	Val	Leu	Val		Leu	Val	Gly	Met	Gly	
	80					85		^		~~~	90					95	
	TTA	GGA	ATG	TAT	CAA	CTC	TTT Phe	CAT	CTA	CAG	AAG	GAA	CTG	GCA	GAA	CTC	406
	beu	GIY	Mer	ΙΫ́Ι	100	reu	Fne	nis	Leu	105	rys	GIU	ren	нта	110	Leu	
20	CGT	GAG	TTC	ACC		CAC	AGC	CTT	AGA		TCA	TCT	TTT	GAA		CAA	454
	Arg	Glu	Phe	Thr	Asn	His	Ser	Leu	Arg	Val	Ser	Ser	Phe	Glu	Lvs	Gln	
				115					120			•		125	_		
							CCC										502
	Ile	Ala		Pro	Ser	Thr	Pro		Glu	Thr	Lys	Lys		Arg	Ser	Val	
25	GCC	CAC	130	202	ccc	**	ccc	135	TTC X	***	mcc	3 mc	140	cmc	C 3 3	mcc	E E A
							Pro										550
		145			047		150			9	501	155		Dea	GIU	115	
	GAA	GAC	ACA	TAT	GGA	AÇT	GCT	TTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	AAA	598
		Asp	Thr	Tyr	Gly	Thr	Ala	Leu	Ile	Ser	Gly	Val	Lys	Tyr	Lys	Lys	
30	160					165					170					175	
							GAG										646
	GIA	GIĀ	reu	vaı	180	ASI	Glu	Ala	GIA	185	Tyr	Pué	Val	Tyr	5er	гля	
	GTA	TAC	TTC	CGG		CAG	TCT	TGC	AAC		CAG	ccc	СТА	AGC		AAG	694
							Ser										0,73
35				195	-			-	200					205		-	
	GTC	TAT	ATG	AGG	AAC	TTT	AAG	TAT	CCT	GGG	GAT	CTG	GTG	CTA	ATG	GAG	742
	Val	Tyr		Arg	Asn	Phe	Lys		Pro	Gly	Asp	Leu		Leu	Met	Glu	
	GAG	AAC	210	TTC	አአጥ	TT A C	TGC	215	N/CTP	ccc	CAC	202	220	ccc	CNC	».cc	790
40							Cys										, 50.
40		225	-,0			-1-	230			01,	0.2	235		niu	****	001	
	AGC	TAC	CTA	GGG	GCA	GTA	TTT	AAT	CTT	ACC	GTT		GAC	CAT	TTA	TAT	838
	Ser						Phe										
	240				_	245					250					255	
45	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	886
~~	val	ASD	тте	ser	Gin 260	Leu	Ser	ren	тте		rne	GIU	GIU	ser		Tnr	
	TTT	ттт	GGC	тта		AAG	CTT	TAAA	GGAZ	265	יערטי	י מידי די	G A	ጥርልጥ	270 כדאר	,	937
		Phe						****						···	O.M.	•	,,,
		-		275			278										
50	TATI	CTTT	'AT C	ATG	ATGC	C AG	GAAT	ATTG	TCI	TCAA	TGA	GAGI	CTTC	TT A	AGAC	CAATT	997

	GAG	CCAC.	MAA '	GACC	MUMAL	3G I	CCAA	CAGG.	LCA	GCIA	CCCI	ICA	1111	CTA	GAGGI	CCAIG	1037
	GAG:	IGGI	CCT '	TAAT	GCCT	C A	TCAT	GAGC	AG.	ATGG	GAAG	AAG	ACTG	TTC	CTGAG	GAACA	1117
5	TAA	AGTT'	TTG (GGCT	GCTGT	G T	GGCA	ATGC	A GA	GGCA	AAGA	GAA	GGAA	CTG	TCTGA	TGTTA	1177
	AAT	GGCC:	AAG :	AGCA:	TTTT	AG C	CATT	GAAG	A AA	AAAA	AAAC	CTT	TAAA	СТС	ACCTT	CCAGG	1237
	GTG	GGTC'	TAC '	TTGC:	TACCI	C A	CAGG	AGGC	GT	CTTT	TAGA	CAC	ATGG'	TTG	TGGTA	TGACT	1297
10	ATA	CAAG	GGT (GAGA	AAGG/	AT G	CTAG	GTTT	TA C	GGAT.	AAGC	TAG	AGAC'	TGA	AAAAA	GCCAG	1357
	TGT	CCCA	TTG (GCAT	CATC	T T	'ATTT	TAAC	TG.	ATGT	TTTC	TGA	GCCC.	ACC	TTTGA	TGCTA	1417
•	ACA	GAGA	AAT .	AAGA	GGGGT	G T	TTGA	GGCA	AA	GTCA	TTCT	CTA	CATA	GCA	TGTGT.	ACCTC	1477
15	CAG	rgca.	ATG .	ATGT	CTGT	ST G	TGTT	TTTA	GT.	ATGA	GAGT	AGA	GCGA'	TTC	TAAAG	AGTCA	1537
	CAT	GAGT	ACA :	ACGC	GTACA	AT T	ACGG	AGTA	AT.	ATTA	GAAA	CGT	ATGT	GTT	ACATT	TGATG	1597
	CTA	GAAT	ATC '	rgaa:	rgtti	с т	TGCT	A								÷	1623
20														•			
	(2)	INF	ORMA'	rion	FOR	SEQ	ID i	NO:2	5 :								
		(i	-				CTER		cs:								
25				-			26 ba		i								
							ESS:		gle								
		(i,					line cDl:		mR	NA							
		(i·		EATU		TNE	'ORMA'	r T (NI :	. 67	~e	1 6						
30		(v)			AL SC			IION	: E1		13						
				A) hi	uman TRAIN	١.							,				
		(v:		•	IATE		RCE:										
		(v					L-hFI SCRIE		J - C1	FO T	י אי	26					
35		,,,	,	UDQ.						1 4	.,,,					1.4	
															AGGC	14	
	AAG	TCC	AAC	TCA	AGG	TCC	ATG Met	CCT	CTG	GAA	TGG	GAA	GAC	ACC		56	
40				155					160				_	165			
	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	GTG	AAG	TAT	AAG	AAG	GGT	GGC	101	
					180					175					180		
							GGG									146	
45					185		Gly		_	190		-		•	195		
							TGC									191	
	Tyr	Phe	Arg	Gly	Gln 200	Ser	Cys	Asn	Asn	Leu 205	Pro	Leu	Ser	His	Lys 210	•	
	GTC	TAC	ATG	AGG		TCT	AAG	TAT	ccc		GAT	CTG	GTG	ATG		236	

	Val	Tyr	Met	Arg	Asn 215	Ser	Lys	Tyr	Pro	Gln 220	Asp	Leu	Val	Met	Met 225		
_		GGG Gly														281	
5		AGC Ser			CTG Leu					AAT Asn					GAT Asp	326	
		TTA Leu														371	
10	GAA	·. TCT	CAG		-260 TTT	ጥጥር	GGC	ጥጥል	ጥልጥ	265	CTC	ተነኳ አ	GAG	A A C C	270 NCT	407	
		Ser			Phe					Lys	Leu	1	one:	2100	no i		
	TTG	GGAT'	rc		275					280	281					426	
15	(2)	INF	ORMA?	NOI	FOR	SEQ	ID I	NO : 2	7:								
20		(i:	() () () (i) M(v) FE	QUENCA) LE B) TY C) ST C) TC C) TC C) EATUR	ENGTH (PE: (RANI)POLO (JLE) (RE:	H: 24 nucl DEDNI DGY: TYPE:	laic ESS: line ger	acio sinq ear netio	i jle DN		16	10			,		
25			ORI () (E L) IN	(GINA A) hi B) ST MMEDI C) CI	AL SO man TRAIN TATE	OURCE N: SOUE	E: RCE:	1110	v. F.	.63.	10			•			
30				NFOF SEQU						Q II	ONO:	: 27					
	AATT	[ATA]	ATG T	'ATA	\AAAA	AG CA	ATGC	\ATT <i>i</i>	TA?	ATTC	ATAA	AAT	TATAC	GCC (CCACTO	GACCA	60
	TTCT	CCTC	STA C	CTG	GAGC	A GI	TCAC	CACTA	ACA	AGGGG	TAT	ACC	CCAT	rgc :	rgacc:	rgctc	120
35	TGC	AGGAT	rcc c	AGGA	AGGI	G AG	CAT	AGCCI	AC1	AACC	CTGT	TTG	GTAC	GCA (CAGCG	ACAGC	180
	AACI	rgage	scc 1	TGA	\GGC1	G TI	TATCE	GAAA	ATI	GTG	GCG	GAAA	CTTC	CA (GGGT	TGCT	240
	CTGA	AGCTI	CT 1	GAGG	CTTC	T CA	GCTI	CAGO	TGC	AAAC	TGA	GTGC	GTGT	TT (CTTTG	AGAAG	300
40	CAGA	ATC	AGA G	AGAG	AGAG	A TA	GAGA	LAAGA	GAA	AGAC	AGA	GGT	STTTC	cc 1	TAGCT	ratgg	360
	AAAC	CTCTA	ATA A	GAGA	GATO	C AG	CTT	CCTC	CTC	TTGA	AGCA	GTC	GCA	CA C	GGTC	CCGTC	420
45	CTTG	SACAC	CT C	AGCC	TCTA	C AG	GACT	GAGA	AGA	AGTA	AAA	CCGT	TTGC	TG (GGCT	GCCT	480
4 5	GACT	CACC	AG C	TGCC	Met		_		Phe					Pro	CAG Gln		531
	TAC	TGG	GTG	GAC	AGC	AGT	GCC	AGC	5 TCT	ccc	TGG	GCC	CCT	CCA	GGC F	ACA	579

	Tyr	Trp	Val 15	Asp	Ser	Ser	Ala	Ser 20	Ser	Pro	Trp	Ala	Pro 25	Pro	Gly	Thr	
	GTT	CTT	CCC	TGT	CCA	ACC	TCT	GTG	CCC	AGA	AGG	CCT	GGT	CAA	AGG	AGG	627
5		30			Pro		35					40				_	
•	CCA	CCA	CCA	CCA	CCG	CCA	CCG	CCA	CCA	CTA	CCA	CCT	CCG	CCG	CCG	CCG	675
	45				Pro	50					55					60	
	CCA	CCA	CTG	CCT	CCA	CTA	CCG	CTG	CCA	CCC	CTG	AAG	AAG	AGA	GGG	AAC	723
10					Pro 65					70					75		
	CAC	AGC	ACA	GGC	CTG	TGT	CTC	CTT	GTG	ATG	TTT	TTC	ATG	GTT	CTG	GTT	771
	His	Ser	Thr	Gly 80	Leu	Cys	Leu	Leu	Val 85	Met	Phe	Phe	Met	Val 90	Leu	Val	
	GCC	TTG	GTA	GGA	TTG	GGC	CTG	GGG	ATG	TTT	CAG	CTC	TTC	CAC	CTA	CAG	819
15			95		Leu			100					105				
	AAG	GAG	CTG	GCA	GAA	CTC	CGA	GAG	GTA	GCCI	rgc (CGGC	AGACT	rg Ct	rgrgo	CCTG	873
		110			Glu		115										
	GAG	GCACC	CAG (GCAT!	AAGGG	G A	rgga(GGCC	CAC	TGCC	TGG	С	• • • •	• •	GAT	TCTGC	92
20	CTC	TTTT	SCT 1	DAAAT	SAATT	T T	ATTT	TATI	ATA	CATO	TTT	TCT	CTTTC	TG 1	TTTT?	ACTAG	98
	TCT	ACC	AGC	CAG	ATG	CAC	ACA	GCA	TCA	TCT	TTG	GAG	AAG	CAA	ATA	G	102
	Ser	Thr	Ser	Gln 120	Met	His	Thr	Ala	Ser 125	Ser	Leu	Glu	Lys	Gln 130	Ile	G	101
25	GTG	AGTCI	TTT 7	TTTC	CATG	T AC	ATTO	SAGTI	ccc	AAAC	ATG	ATC	TCAG		CAGAA	CTATG	108
	TTA	ATGGA	LAT (CCTI	TAAAT	T CI	GTCC	CACA	CTI	TGG1	TTC	TGTA	CACI	'AT A	AGAC	GAATT	1148
	C		•••		TTCCC.	A CC	AAAA	TAAT	AGT	TGÇT	'ÀTT	TCAT	TTTA	AC F	ATATA	TTTTT.	119
30	CCTC	CTCTC	TA 1	GAT	ACAG	•											1213
	ly F	lis P	ro S	Ser F .35	CA C	ro P	ro G	ilu L 1	ys L 40	ys G	lu I	Leu A	rg I	ys V .45	/al A	CC la	1260
35		TTA Leu			CTGT	ATCI	' GGA	AGGT	ACA	GGŢĢ	AGAT		• • • •	• • • •	•		1298
		TGCA		GAGA	AGAT	G GA	CCAG	ATGG	TCC	CTAA	GAT	CCTT	CCCA	AC I	TTAG	AACTT	1355
	TAGA	GTTC	CT I	'GGA1	TTGG	C TI	TTTC	CTTC	AGG	AAAG	GAC	TTCA	AAGC	CT A	GCAG	ATTTG	1415
40	GTGC	TAGT	TC 1	GAAG	ATAG:	T AA	AATC	TTTG	TTC	CAGA	GAG	CAAA	TATT	TT C	TCAA	TAATT	1475
	TCTT	'ACTG	CA A	TGGA	TTAC	G GG	TATA	TACT	ATT	GTTC	CAA	TTGT	GTGG	AT G	ACAA	AATAG	1535
45			•													TCTAT	
																TTAGA	
	AACT	TAGT	TT G	TTGG	ATGC	A TG	ACTA	ጥጥርር	TTG	CTGA	AAG	CTCC	ተውውጥ	CC A	ተጥጥ አ	ጥጥጥር Δ	1715

																TAT	1763
	Τ.7	LAS	s Ser	Asr	1 Ser 155		Ser	Met	Pro	Leu 160		ı Trp	Glu	ı Asp	7 Thi	Tyr 5	
	GGA	ATT	GTC	CTG	CTT	TCT	GGA	GTG	AAG	TAT	AAG	AAG	GGT	GGC	CTT	GTG	1811
5						Ser											
						CTG			GTA					TAC			1859
	Ile	Asn	Glu 185	Thr	Gly	Leu		Phe 190	Val	Tyr	Ser	Lys	Val 195	Tyr	Phe	Arg	
	GGT	CAA	TCT	TGC	AAC	AAC	CTG	CCC	CTG	AGC	CAC	AAG	GTC	TAC	ATG	AGG	1907
10	-	200		•			205					210				-	
						CAG											1955
	Asn 215	Ser	Lys	Tyr	Pro	Gln 220	Asp	Leu	Val	Met	Met 225	Glu	Gly	Lys	Met	Met 230	
						GGG											2003
15			•		235	Gly				240	ı				245		
						ACC											2051
				250		Thr			255			-		260			
20																TTA	2099
£ U			265			Asn		270					275	•	-	Leu	
				TAA	GAGA	LAGCA	CT T	TGGG	ATTC	T TT	CCAT	TATO	ATI	CTTI	GTT		2151
	Tyr	Lys	Leu 281														
25	ACAC	GCAC	CCG A	GAAT	GTTG	T AT	TCAG	TGAG	GGT	CTTC	TTA	CATG	CATI	TG A	GGTC	CAAGTA	2211
	AGAZ	AGACA	ATG A	ACCA	AGTG	G AC	CTTG	AGAC	CAC	AGGG	TTC	AAAA	TGTC	TG I	AGCI	CCTCA	2271
								•					•			SAACTC	
30	TGGG	CTGC	CA 1	'GTGP	AGAG	G GA	GAAG	CATG	AAA	AAGC	AGC	TACC	AGGT	GT I	CTAC	CACTCA	
	TCTT	AGTO	SCC I	'GAGA	GTAI	T TA	GGCA	GATT	GAA	.AAGG	ACA	cc					2433
	(2)	INFO	RMAT	ION	FOR	SEQ	ID N	0:28							•		
35 •	-	(i)	(A) LE	NGTH	IARAC I: 17	07 b	ases									
	*.		(0) SI	RAND	nucl EDNE	ss:	sing									
			-	-		GY:				_							
40						YPE:	CDN.	A to	mRN	A							
~		(17	r) FE			INF	^pwn	TT∩N		ce	22_2	. 4				•	
		(v)	ORI	GINA	L SC	URCE		† 10M		GS.	23-2	. 4					
		(vi	•	.) mc MEDI		SOUR	CE:										
		,				λMF.		λMF1.	18								
45		(vi	•	•		DES	•			מד ס	ŇO.	28					
		,	- - ,	20													

CTGCGGAAAC TTTATAAAGA AAACTTAGCT TCTCTGGAGC AGTCAGCGTC AGAGTTCTGT

	CCTTGACACC TGAGTCTCCT CCACAAGGCT GTGAGAAGGA AACCCTTTCC TGGGGCTGGG 1												120				
5	TGCC		Glr				Asr					Glr				GTA Val 15	169
	GAC Asp	AGC Ser	AGT Ser	GCC Ala	ACT Thr 20	TCA Ser	TCT Ser	TGG Trp	GCT Ala	CCT Pro 25	CCA Pro	GGG Gly	TCA Ser	GTT Val	TTT Phe 30	CCC Pro	217
10	TGT Cys	CCA. Pro	TCT Ser	TGT Cys 35	GGG Gly	CCT Pro	AGA Arg	GGG Gly	CCG Pro 40	GAC Asp	CAA Gln	AGG Arg	AGA Arg	CCG Pro 45	CCA Pro	CCT Pro	265
				CCT	GTG Val				CCA								313
15			CCA		ACC Thr			AAG									361
	TGG Trp 80	CTA	CCG Pro	GTG Val	GTA Val	TTT Phe 85	TTC	ATG Met	GTT Val	CTG Leu	GTG Val 90	GCT	CTG Leu	GTT Val	GGA Gly	ATG Met 95	409
20	GGA				TAT	CAG				Leu	CAG				Ala	GAA	457
			Glu	Phe	100 ACC Thr				Leu					Phe			505
25	CAA Gln	ATA Ile	GCC Ala	115 AAC Asn	CCC Pro	AGT Ser	ACA Thr	Pro	120 TCT Ser	GAA Glu	AAA Lys	AAA Lys	Glu	125 CCG Pro	AGG Arg	AGT Ser	553
		Ala			ACA Thr		Asn					Ser					601
30	TGG Trp	145 GAA Glu	GAC Asp	ACA Thr	TAT Tyr	GGA Gly	150 ACC Thr	GCT Ala	CTG Leu	ATC Ile	TCT Ser	155 GGA Gly	GTG Val	AAG Lys	TAT Tyr	AAG Lys	649
					GTG Val												697
35	AAA	GTA	TAC	TTC	180 CGG Arg	GGT	CAG	TCT	TGC	185 AAC	AAC	CAG	ccc	CTA	190 AAC	CAC	745
•	AAG	GTC	TAT	195 ATG	AGG Arg	AAC	TCT	AAG	200 TAT	ССТ	GAG	GAT	CTG	205 GTG	СТА	ATG	793
40	GAG	GAG	210 AAG	AGG	TTG Leu	AAC	TAC	215 TGC	ACT	ACT	GGÄ	CAG	220 ATA	TGG	GCC	CAC	841
	AGC	225 AGC	TAC	CTG	GGG	GCA	230 GTA	TTC	ААТ	CTT	ACC	235 AGT	GCT	GAC	CAT	TTA	889
45	240 TAT	GTC	AAC	ATA	TCT	245 CAA	CTC	TCT	CTG	ATC	250 AAT	TTT	GAG	GAA	тст	255 AAG	937
					Ser 260 TTG					265					270	Lys	984
					Leu												

			•				
	GATCTACTAT	275 TCTTTATCAT	279 GGGCACCAGG	AATATTGTCT	TGAATGAGAG	TCTTCTTAAG	1044
	ACCTATTGAG	ATTAATTAAG	ACTACATGAG	CCACAAAGAC	CTCATGACCG	CAAGGTCCAA	1104
5	CAGGTCAGCT	ATCCTTCATT	TTCTCGAGGT	CCATGGAGTG	GTCCTTAATG	CCTGCATCAT	1164
	GAGCCAGATG	GAAGGAGGTC	TGTGACTGAG	GĞACATAAAG	CTTTGGGCTG	CTGTGTGACA	1224
10	ATGCAGAGGC	ACAGAGAAAG	AACTGTCTGA	TGTTAAATGG	CCAAGAGAAT	TTTAACCATT	1284
10	GAAGAA	GACACCTTTA	CACTCA-CTT	CCAGGGTGGG	TCTACTTACT	ACCTCACAG-	1338
	AGGCCGTTTT	TGAGACATA-	-GTTGTGGTA	TGAATATACA	AGGGTGAGAA	AGGAGGCT-C	1395
15	ATTTGACTGA	TAAGCTAGAG	ACTGAAAAAA	AGACAGTGTC	TCATTGGCAC	CATCTTTACT	1455
	GTTACCTAAT	GTTTTCTGAG	CCGACCTTTG	ATCCTAACGG	AGAAGTAAGA	GGGATGTTTG	1515
	AGGCACAAAT	CATTCTCTAC	ATAGCATGCA	TACCTCCAGT	GCAATGATGT	CTGTGTGT	1573
20	TTGTATGTAT	GAGAGCAAAC	AGATTCTAAG	GAGTCATATA	AATAAAATAT	GTACATTATG	1633
	GAGTACATAT	TAGAAACC	TGTTACAT	TTGATGCTAG	A-TATCTGAA	TGTTTCTTGG	1688
	CAATAAACTC	TAATAGTCT		•			1707
25	(2) INFORM	ATION FOR SI	EQ ID NO:29				
30	(iii) (ii) ! (v) Oi	EQUENCE CHAM (A) LENGTH: (B) TYPE: nu (C) STRANDEM ANTI-SENSEMOLECULE TYM RIGINAL SOUM (A) human	924 bases ucleic acid DNESS: sing : YES PE: DNA				
35	(viii)	SEQUENCE I	DESCRIPTION	: SEQ ID NO	: 29		
	GAATCCCAAA	GTGCTTCTCT	TAGAGCTTAT	ATAAGCCGAA	AAACGTCTGA	50	
	GATTCCTCAA	AATTGACCAG	AGAGAGCTCA	GATACGTTGA	CATATAAATG	~100	
40	ATCAGCACTG	GTAAGATTGA	ACACTGCCCC	CAGGTAGCTG	CTGCGGGCCC	150	
	ACATCTGCCC	AGTAGTGCAG	TAGCTCATCA	TCTTCCCCTC	CATCATCACC	200	
	AGATCCTGGG	GATACTTAGA	GTTCCTCATG	TAGACCTTGT	GGCTCAGGGG	250	
45	CAGGTTGTTG	CAAGATTGAC	CCCGGAAGTA	TACTTTGGAA	TATACAAAGT	300	

50

55

ACAGCCCAGT TTCATTGATC ACAAGGCCAC CCTTCTTATA CTTCACTCCA 350
GAAAGCAGGA CAATTCCATA GGTGTCTTCC CATTCCAGAG GCATGGACCT 400

	TGAGTTGGAC TTGCCTGTTA AATGGGCCAC TTTCCTCAGC TCCTTTTTTT	450
. 5	CAGGGGTGG ACTGGGGTGG CCTATTTGCT TCTCCAAAGA TGATGCTGTG	500
5	TGCATCTGGC TGGTAGACTC TCGGAGTTCT GCCAGCTCCT TCTGTAGGTG	550
	GAAGAGCTGA AACATCCCCA GGCCCAATCC TACCAAGGCA ACCAGAACCA	600
10	TGAAAAACAT CACAAGGAGA CACAGGCCTG TGCTGTGGTT CCCTCTCTTC	650
	TTCAGGGGTG GCAGCGGTAG TGGAGGCAGT GGTGGCGGCG GCGGCGGAGG	700
	TGGTAGTGGT GGCGGTGGCG GTGGTGGTGG TGGCCTCCTT TGACCAGGCC	750
15	TTCTGGGCAC AGAGGTTGGA CAGGGAAGAA CTGTGCCTGG AGGGGCCCAG	800
	GGAGAGCTGG CACTGCTGTC CACCCAGTAG ATCTGGGGAT ATGGGTAATT	850
	GAAGGGCTGC TGCATGGCAG CTGGTGAGTC AGGCCAGCCC CAGCAAACGG	900
20	TTTTACTTCT TCTCAGTCCT GTAG	924
	(2) INFORMATION FOR SEQ ID NO:30	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 924 bases (B) TYPE: ribonucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: RNA (iii) ANTI-SENSE: YES (v) ORIGINAL SOURCE: (A) human	
35	(viii) SEQUENCE DESCRIPTION: SEQ ID NO:30	
	GAAUCCCAAA GUGCUUCUCU UAGAGCUUAU AUAAGCCGAA AAACGUCUGA	50
. ,	GAUUCCUCAA AAUUGACCAG AGAGAGCUCA GAUACGUUGA CAUAUAAAUG	100
40	AUCAGCACUG GUAAGAUUGA ACACUGCCCC CAGGUAGCUG CUGCGGGCCC	150
	ACAUCUGCCC AGUAGUGCAG UAGCUCAUCA UCUUCCCCUC CAUCAUCACC	200
	AGAUCCUGGG GAUACUUAGA GUUCCUCAUG UAGACCUUGU GGCUCAGGGG	250
45	CAGGUUGUUG CAAGAUUGAC.CCCGGAAGUA UACUUUGGAA UAUACAAAGU	300
	ACAGCCCAGU UUCAUUGAUC ACAAGGCCAC CCUUCUUAUA CUUCACUCCA	350
50	GAAAGCAGGA CAAUUCCAUA GGUGUCUUCC CAUUCCAGAG GCAUGGACCU	400
	UGAGUUGGAC UUGCCUGUUA AAUGGGCCAC UUUCCUCAGC UCCUUUUUUU	450

CAGGGGGUGG ACUGGGGUGG CCUAUUUGCU UCUCCAAAGA UGAUGCUGUG 500

_	UGC	AUCU	GGC	UGGU	AGAC	UC 1	UCGGA	GUUC	U GC	CAGC	שככש	טכט	IGUAG	GUG	550	
5	GAA	GAGC	UGA	AACA	uccc	CA (GGCCC	AAUC	C UA	CCAA	GGCA	ACC	AGAA	.CCA	600	
	UGA	AAAA	.CAU	CACA	AGGA	GA (CACAG	GCCU	G UG	CUGU	GGUU	ccc	UCUC	UUC	650	
10	υυC	AGGG	GUG	GCAG	CGGU	AG (UGGAG	GCAG	U GG	UGGC	GGCG	GCG	GCGG	AGG	700	
	UGG	UAGU	GGU	GGCG	GUGG	CG (GUGGU	GGUG	G UG	GCCU	CCUU	UGA	CCAG	GCC	750	
	UUC	UGGG	CAC	AGAG	GUUG	GA (CAGGG	AAGA	A CU	GUGC	CUGG	AGG	GGCC	CAG	800	
15	GGA	GAGC	UGG	CACU	GCUG	uc (CACCC	AGUA	g au	CUGG	GGAU	AUG	GGUA	AUU	850	
	GAA	GGGC	UGC	UGCA	UGGC.	AG (CUGGU	GAGU	C AG	GCCA	.GCCC	CAG	CAAA	CGG	900	
	טטט	UACU	υςυ	ucuc	AGUC	כט (GUAG								924	
20																
25 30		(ii (ii (iv (v)	(A) (B) (C) (D)) MO i) A) FR (A) i) F (D)	LEN TYP STR TOP LECU NTI- AGME GINA hum EATU OTH	GTH: e: n ANDN OLOG ILAR SENSI NT T L SO an RE ER II	924 ucle ESS: Y: 1 TYE E: N YPE: URCE	:	es cid ble r DNA	to m	mid		hFL1				
35												CT	ACAG	GACT		10
	GA	GAAG.	AAGT	AAA	ACCG:	TTT	GCTG	GGGC'	rg g	CCTG.	ACTC.	A CC	AGCT	GCC		5
	ATG	CAG	CAG	ccc	TTC	AAT	TAC	CCA	TAT	ccc	CAG	ATC	TAC	TGG	GTG	10
40 .	GAC	AGC	AGT	GCC	AGC	TCI	ccc	TGG	GCC	CCT	CCA	GGC	ACA	GTT	CTT	14
	ccc	TGT	CCA	ACC	TCT	GTG	ccc	AGA	AGG	CCT	GGT	CAA	AGG	AGG	CCA	194
4 5	CCA	CCA	CCA	CCG	CCA	CCG	CCA	CCA	CTA	CCA	ССТ	CCG	CCG	CCG	CCG	239
	CCA	CCA	CTG	CCT	CCA	CTA	CCG	CTG	CCA	ССС	CTG	AAG	AAG	AGA	GGG	284
	AAC	CAC	AGC	ACA	GGC	CTG	TGT	CTC	CTT	GTG	ATG	TTT	TTC	ATG	GTT	329
50	CTG	GTT	GCC	, TTG	GTA	GGA	TTG	GGC	CTG	GGG	ATG	ттт	CAG	СТС	TTC	374
	CAC	СТА	CAG	AAG	GAG	CTG	GCA	GAA	CTC	CGA	GAG	TCT	ACC	AGC	CAG	419

	ATG	CAC	ACA	GCA	TÇA	TCT	TTG	GAG	AAG	CAA	ATA	GGC	CAC	CCC	AGT	464
_	CCA	ccc	CCT	GAA	AAA	AAG	GAG	CTG	AGG	AAA	GTG	GCC	CAT	TTA	ACA	509
5	GGC	AAG	TCC	AAC	TCA	AGG	TCC	ATG	CCT	CTG	GAA	TGG	GAA	GAC	ACC	554
	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	GTG	AAG	TAT	AAG	AAG	GGT	GGC	599
10	CTT	GTG	ATC	AAT	GAA	ACT	GGG	CTG	TAC	TTT	GTA	TAT	TCC	AAA	GTA	644
	TAC	TTC	CGG	GGT	CAA	TCT	TGC	AAC	AAC	CTG	CCC	CTG	AGC	CAC	AAG	689
	GTC	TAC	ATG	AGG	AAC	TCT	AAG	TAT	ccc	CAG	GAT	CTG	GTG	ATG	ATG	734
15	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	ACT	ACT	GGG	CAG	ATG	TGG	GCC	779
	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	TTC	AAT	CTT	ACC	AGT	GCT	GAT	824
	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	CTC	TCT	CTG	GTC	AAT	TTT	GAG	869
20	GAA	TCT	CAG	ACG	TTT	TTC	GGC	TTA	TAT	AAG	CTC	TAA	GAG	AAGC	ACT	915
	TTG	GATI	rc													924
25 30	(2)	(i) (ii) (iv)	SEQUANCE (A) (B) (C) (D) (D) MOI i) AI i) FRI	IION LENG Type STRA TOPO LECU: NTI-S AGMEN OTHE	E CHA ETH: ANDNI CLOG! LAR SENSI RE	ARACT 927 ICles ICSS: C: 1: TYPE CPE	reris base ic ac inear	STIC: es cid r ONA t	5:	RNA						
35		(ix)		QUENC					SEQ`I	ID NO	0:32					
							GAG	AAGG?	AA(CCTI	TCC	TGGC	GCT	GG G	rgcc	32
	ATG	CAG	CAG	CCC.	ATG	AAT	TAC	CCA	TGT	CCC	CAG	ATC	TTC	TGG	GTA	77
40	GAC	AGC	AGT	GCC	ACT	TCA	TCT	TGG	GCT	CCT	CCA	GGG	TCA	GTT	TTT	122
	ccc	TGT	CCA	TCT	TGT	GGG	CCT	AGA	GGG	ĊCG	GAC	CAA	AGG	AGA	CCG	167
45	CCA	CCT	CCA	CCA	CCA	CCT	GTG	TCA	CCA	CTA	CCA	CCG	CCA	ŢCA	CAA	212
	CCA	CTC	CCA	CTG	CCG	CCA	CTG	ACC	CCT	CTA	AAG	AAG.	AAG	GAC	CAC	257
	AAC	ACA	AAT	CTG	TGG	CTA	CCG	GTG	GTA	TTT	TTC	ATG	GTT	CTG	GTG	302
50	GCT	CTG	GTT	GGA	ATG	GGA.	TTA	GGA	ATG	TAT	CAG	CTC	TTC	CAC	CTG	347
	CAG	AAG	GAA	CTG	GCA	GÄA	CTC	CGT	GAG	TTC	ACC	AAC	CAA	AGC	CTT	392

	AAA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	ATA	GCC	AAC	ccc	AGT	ACA	CCC	437
5	TCT	GAA	AAA	AAA	GAG	CCG	AGG	AGT	GTG	GCC	CAT	TTA	ACA	GGG	AAC	482
J	CCC	CAC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	527
•	ACC	GCT	CTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	AAA	GGT	GGC	CTT	GTG	572
10	ATC	AAC	GAA	ACT	GGG	TTG	TAC	TTC	GTG	TAT	TCC	AAA	GTA	TAC	TTC	617
	CGG	GGT	ĆÃG	TCT	TGC	AAC	AAC	CAG	ссс	CTA	AAC	CAC	AAG	GTC	TAT	662
	ATG	AGG	AAC	TCT	AAG	TAT	CCT	GAG	GAT	CTG	GTG	СТА	ATG	GAG	GAG	707
15	AAG	AGG	TTG	AAC	TAC	TGC	ACT	ACT	GGA	CAG	ATA	TGG	GCC	CAC	AGC	752
	AGC	TAC	CTG	GGG	GCA	GTA	TTC	AAT	CTT	ACC	AGT	GCT	GAC	CAT	TTA	797
	TAT	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	842
20	AAG	ACC	TTT	TTC	GGC	TTG	TAT	AAG	CTT	TAA	AAG	AAAA	AGC I	ATTT:	TAAAAT	892
	GAT	CTACT	FAT :	rctt:	PATC	AT GO	GCA	CAG	AA:	TAT						927
25	(2)		SEQUAL (A)	TION JENCI LENC Type STRI	E CHI GTH: e: nu	ARACT 20 k uclei	TERIS	STICS								
30		(iii) (iv)	(D) MOI Al FRI	TOPOLECU: NTI-S AGMEN	DLOGY LLAR SENSI	Y: li TYPE E: YPE:	E: O1		nuc	leic	acio	i			-	
35			(B) (C) (D) (E)	STRA IND: DEVI TISS CELI	ELOPN SUE :	ÆNT <i>!</i> CYPE :	AL S		:							
40		•	(A) (B)	CELI MEDIA LIBI CLON	ATE S RARY NE:		CE:							ı		
45	САТТ	(ix)	(D) SE(EATUR OTHE QUENC	ER IN	ESCRI	PTIC		SEQ I	ED NO):33					
								10.2								
50	(2)		SEQUAL (A)	TION JENCE LENG Type STRA	E CHA STH: e: nu	ARACT 37 b aclei	TERIS Dases	STICS								

5	(D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN:
10	(C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY
15 .	(A) LIBRARI (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: (ix) SEQUENCE DESCRIPTION: SEQ ID NO:34
20	ATGCGGCCGCTGGATCCTTTGTATGAAATTGAGTAAT 37 (2) INFORMATION FOR SEQ ID NO:35 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 bases
25	(B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE:
30	 (v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE:
35	(E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE:
40	<pre>(vii) FEATURE (D) OTHER INFORMATION: sense primer 1 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:35</pre>
	ATGCCCAAGTGACTGACATCAACT 24
4 5	(2) INFORMATION FOR SEQ ID NO:36 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 50 bases (B) Type: nucleic acid (C) STRANDNESS:
50	<pre>(D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: YES</pre>

5	(iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE:	
10	(F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE:	
F	<pre>(vii) FEATURE (D) OTHER INFORMATION: anti-sense primer 1</pre>	
15	(xi) SEQUENSE DESCRIPTION: SEQ ID NO:36	
	GCGCGGATCCAGGAAGTGGGAAAGGATTACCTTCCTCTTTGCACTTGGTG	50
20	(2) INFORMATION FOR SEQ ID NO:37 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 10 bases (B) Type: nucleic acid (C) STRANDNESS:	
25	 (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) rat, mouse, human 	
30	(B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE:	
35	(G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: 19 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:37	
40	CCAGCCATGG 10	
4 5	(2) INFORMATION FOR SEQ ID NO:38 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) Type: nucleic acid (C) STRANDESS: single (D) TOPOLOGY: linear	
50	(ii) MOLECUILAR TYPE: Other nucleic acid(iii) ANTI-SENSE: NO(iv) FRAGMENT TYPE:(v) ORIGINAL SOURCE:(A)	

	·
5	(B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE:
10	(A) LIBRARY (B) CLONE:hybridoma d10S-2 (vii) FEATURE (D) OTHER INFORMATION: sense primer 2 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:38
	AAGACCACAAGGTCCAACAG 20
15	(2) INFORMATION FOR SEQ ID NO:39 (i) SEQUENCE CHARACTERISTICS:
20	 (A) LENGTH: 20 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO
25	(iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE:
30 ·	(E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY
35	(B) CLONE:hybridoma d10S-2 (vii) FEATURE (D) OTHER INFORMATION: sense primer 3 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:39
	GGTGAGAAAGGATGCTAGGT 20
40	(2) INFORMATION FOR SEQ ID NO:40 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) Type: nucleic acid
45	<pre>(C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE:</pre>
50	(v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE:

```
(E) TISSUE TYPE:
                      (F) CELL TYPE:
                      (G) CELL LINE:
                  (vi) IMMEDIATE SOURCE:
                      (A) LIBRARY
                      (B) CLONE: hybridoma d10S-2
                  (vii) FEATURE
                      (D) OTHER INFORMATION: anti-sense primer 2
                  (ix) SEQUENCE DESCRIPTION: SEQ ID NO:40
10
            CATGGATAAGCTAGAGACTG
                                     20.
             (2) INFORMATION FOR SEQ ID NO:41
                  (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 20 bases
                      (B) Type: nucleic acid
15
                      (C) STRANDNESS: single
                      (D) TOPOLOGY: linear
                  (ii) MOLECUILAR TYPE: Other nucleic acid
                  (iii) ANTI-SENSE: YES
                  (iv) FRAGMENT TYPE:
20
                  (v) ORIGINAL SOURCE:
                      (A)
                      (B) STRAIN:
                      (C) INDIVIDUAL ISOLATE:
                      (D) DEVELOPMENTAL STAGE:
                      (E) TISSUE TYPE:
25
                      (F) CELL TYPE:
                      (G) CELL LINE:
                  (vi) IMMEDIATE SOURCE:
                      (A) LIBRARY
                      (B) CLONE: hybridoma d10S-2
30
                  (vii) FEATURE
                      (D) OTHER INFORMATION: anti-sense primer 3
                  (ix) SEQUENCE DESCRIPTION: SEQ ID NO:41
             GTACAACGCGTACATTACGG 20
35
             (2) INFORMATION FOR SEQ ID NO: 42
                  (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 967 bases
                      (B) Type: nucleic acid
                      (C) STRANDNESS:
                      (D) TOPOLOGY:
                  (ii) MOLECUILAR TYPE:
                 (iii) ANTI-SENSE: NO
                 (iv) FRAGMENT TYPE:
                 (v) ORIGINAL SOURCE:
45
                      (A)
                      (B) STRAIN:
                      (C) INDIVIDUAL ISOLATE:
                      (D) DEVELOPMENTAL STAGE:
                      (E) TISSUE TYPE:
                      (F) CELL TYPE:
50
                     (G) CELL LINE:
```

	<pre>(vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE</pre>														•		
5		(vi	i) Fl	EATU	RE	VEOD!	43 M T	ON			-m12	4 16					
	•	(ix)		OTHI OUEN								4-12					
									AG	GAGG	AA A	CCCT	TTCC'	r GG	GCT	GGGT	70
10	GCC	ATG	CAG	CAG	ссс	GTG	AAT	TAC	CCA	TGT	ccc	CAG	ATC	TAC	TGG	GTA	118
	GAC	AGC	AGT	GCC	ACT	TCT	CCT	TGG	GCT	CCT	CCA	GGG	TCA	GTT	TTT	TCT	166
	TGT	CCA	TCC	TCT	GGG	CCT	AĞA	GGG	CCA	GGA	CAA	AGG	AGA	CCA	CCG	CCT	214
15	CCA	CCA	CCA	CCT	CCA	TCA	CCA	CTA	CCA	CCG	ССТ	TCC	CAA	CCA	ссс	CCG	262
	CTG	CCT	CCA	CTA	AGC	CCT	CTA	AAG	AAG	AAG	GAC	AAC	ATA	GAG	CTG	TGG	310
	CTA	CCG	GTG	ATA	TTT	TTC	ATG	GTG	CTG	GTG	GCT	CTG	GTT	GGA	ATG	GGG	358
20	TTA	GGA	ATG	TAT	CAA	CTC	TTT	CAT	CTA	CAG	AAG	GAA	CTG	GCA	GAA	CTC	406
	CGT	GAG	TTC	ACC	AAC	CAC	AGC	CTT	AGA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	454
	ATA	GCC	AAC	ccc	AGC	AÇA	ССС	TCT	GAA	ACC	AAA	AAG	CCA	AGG	AGT	GTG	502
25	GCC	CAC	TTA	ACA	GGG	AAC	ссс	CGC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	550
	GAA	GAC	ACA	TAT	GGA	ACT	GCT	TTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	AAA	598
30	GGC	GGC	СТТ	GTG	ATC	AAT	GAG	GCT	GGG	TTG	TAC	TTC	GTA	TAT	TCC	AAA	646
30	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AGC	CAG	ССС	CTA	AGC	CAC	AAG	694
	GTC	TAT	ATG	AGG	AAC	TTT	AAG	TAT	ССТ	GGG	GAT	CTG	GTG	CTA	ATG	GAG	742
35	GAG	AAG	AAG	TTG	AAT	TAC	TGC	ACT	ACT	GGC	CAG	ATA	TGG	GCC	CAC	AGC	790
	AGC	TAC	CTA	GGG	GCA	GTA	TTT	AAT	CTT	ACC	GTT	GCT	GAC	CAT	TTA	TAT	838
	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	886
40	ттт	TTT	GGC	TTA	TAT	AAG	CTT	TAA	AGGA	AA A	AGCAT	TTTT	AG A	AŢGAI	CTAI		937
	TATI	CTTT	'AT C	CATGO	ATGO	C AC	GAAT	TATTO	;								967
4 5	(2)	INFC	SEQU (A) (B)	TION JENCE LENG Type STRA	CHA TH:	ARACT 20 b clei	ERIS ases c ac	TICS id									٠
£0.			(D) MOI	TOPO ECUI	LOGY	: li TYPE	near : Ot	•	nucl	.eic	acid	i					

		(vii)										,				
		(ix) S) OTH								4					
		(IX) S	FOOFM	CE DI	LOCK	IF I I	ON:	SEQ	TO M	Ų.4J						
5	AGA	ACTCCGT	GAGTT	CACC	A 2	0										
10	(2)			E CHI GTH:	ARAC'	TERI. base	STIC: s									
		(li) M (iii)	ANTI-	OLOG ILAR SENSI	Y: 1: TYP: E: Y:	inea E: O	r	nuc	leic	aci	d				-	
15		(iv) F (v) OR					•									
20		(A (B (C (D (E) STR) IND) DEV) TIS	AIN: IVIDI ELOPI SUE 1	JAL MENT. TYPE	ISOL AL S		:							•	
		(Vi) I (Vi) (A (B) LIB	L LII ATE : RARY NE:	NE:	CE:										
25		(vii) (D (ix) S) OTH	ER II							rime	r 4				
	CAA'	TATTCCT	GGCAT	CCAT	3 2	0										
30	(2)	(i) SE (A (B	QUENC) LEN) Typ) STR	E CHI GTH: e: ni ANDNI	ARAC' 967 icle: ESS:	reri bas ic a sin	STIC: es cid gle							•		
35		(ii) M (iii) (vii)	ANTI- FEATU) OTH	ILAR SENSI RE ER IN	TYPI E: NO NFORI	E: O O MATIC	ther ON: I	PCR a	ampl	ifie		oduc	ts			
40													A	GAA	CTC	406
	CGT	GAG TT	C ACC	AAC	CAC	AGC	СТТ	AGA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	454
45	ATA	GCC AA	c ccc	AGC	ACA	ccc	TCT	GAA	ACC	AAA	AAG	CCA	AGG	AGT	GTG	502
	GCC	CAC TT	A ACA	GGG	AAC	ccc	CGC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	550
	GAA	GAC AC	A TAT	GGA	ACT	GCT	TTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	AAA	598
50	GGC	GGC CT	T GTG	ATC	AAT	GAG	GCT	GGG	TTG	TAC	TTC	GTA	TAT	TCC	AAA	646

	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AGC	CAG	ccc	CTA	AGC	CAC	AAG	694
	GTC	TAT	ATG	AGG	AAC	TTT	AAG	TAT	CCT	GGG	GAT	CTG	GTG	CTA	ATG	GAG	742
5	GAG	AAG	AAG	TTG	AAT	TAC	TGC	ACT	ACT	GGC	CAG	ATA	TGG	GCC	CAC	AGC	790
	AGC	TAC	CTA	GGG	GCA	GTA	TTT	AAT	CTT	ACC	GTT	GCT	GAC	CAT	TTA	TAT	838
	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	886
10	TTT	TTT	GGC	TTA	TAT	AAG	CTT	TAA	AGGA	AAA A	AGCA:	TTTT	AG A	ATGA:	rcta:	r	937
	TAT	rctti	TA7	CATGO	SATGO	CC AC	GAA?	PATTO	3								967
15	(2)		SEQUAL (A) (B) (C)	JENCI LENC Type STRA	FOR E CHA GTH: E: DI ANDNE	ARACT 191 iclei ESS:	ERIS base ic ac sing	STICS es cid gle									
20		(ii) (iv)	MOI L) AN FRA ORIC (A)	LECUI NTI-S AGMEN SINAI	LLAR SENSE NT TY L SOU	TYPE:	E: Ot		nuc	leic	acio	i					
25			(C) (D) (E) (F)	DEVE TISS CELI	VIDU ELOPN SUE T L TYP	ŒNTA YPE : 'E :	AL ST							,			٠
30		(vii	IMN (A) (B) (B) (D)	EDIA LIBF CLON ATUF OTHE	ATE S RARY IE:	OURC	LATIC	ON: P	CR æ	mpli	fied	i pro	duct	s			
35		(0.00	,02110		JOKI						сстт	TCCT	' GGG	GCTC	GGT	28
	GCC	ATG	CAG	CAG	ccc	GTG	AAT	TAC	CCA	TGT	CCC	CAG	ATC	TAC	TGG	GTA	76
	GAC	AGC	AGT	GCC.	ACT	TCT	CCT	TGG	GCT	CCT	CCA	GGG	TCA	GTT	TTT	TCT	124
40	TGT	CCA	TCC	TCT	GGG	CCT	AGA	GGG	CCA	GGA	CAA	AGG	AGA	CCA	ÇCG	CCT	171
	CCA	CCA	CCA	CCT	CCA	TCA	С										191
4 5	(2)	(i)	SEQU (A) (B) (C) (D)	ENCE LENG Type STRA TOPO	FOR CHA TH: nu LOGY LOGY	RACT 444 clei SS: : li	ERIS base c ac sing near	TICS s id le	i	ai c	م د : م						
50		122/	1.1011		TUT.	TIEE	. 01	W.E.T	HUCL	erc.	aciq						

		(iv)) FR	AGMEI	SENSI NT T L SO	PE:									•		
5			(C) (D) (E)	DEVI	AIN: IVIDI ELOPI SUE '	ÆNT. CYPE	AL S'		:								
10			(G)) IMI (A) (B)	CELI MEDIA LIBI CLOI	L LII ATE S RARY NE:	NE:	CE ;										
15		•	(D)		ER II CE DI							d pro	odic	s			
				•				CGC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	27.
	GAA	GAC	ACA	TAT	GGA	ACT	GCT	TTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	AAA	75
20	GGC	GGC	CTT	GTG	ATC	AAT	GAG	GCT	GGG	TTG	TAC	TTC	GTA	TAT	TCC	AAA	123
	GTA	TAC	TTC	CGG	GGT	CAG	TÇT	TGC	AAC	AGC	CAG	ссс	CTA	AGC	CAC	AAG	171
	GTC	TAT	ATG	AGG	AAC	TTT	AAG	TAT	ССТ	GGG	GAT	CTG	GTG	CTA	ATG	GAG	219
25	GAG	AAG	AAG	TTG	AAT	TAC	TGC	ACT	ACT	GGC	CAG	ATA	TGG	GCC	CAC	AGC	267
	AGC	TAC	CTA	GGG	GCA	GTA	TTT	AAT	CTT	ACC	GTT	GCT	GAC	CAT	TTA	TAT	315
22	GTC	AAC	ATA	TCT	CAA	CTC	TCT	СТG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	363
30	TTT	TTT	GGC	TTA	TAT	AAG	CTT	TAA	AGGA	AAA	AGCAT	TTT?	AG AZ	ATGAT	CTAI	r	414
	TATI	CTT	rat (CATGO	SATGO	C A	GAA:	TATTO	3								444
35	(2)		SEQUAL (A) (B) (C)	JENCE LENC Type STR/	FOR E CHA GTH: E: nu	RACT 28 l cle: SS:	TERIS cases cases cases	STICS sid gle									
40		(iii)	MOI L) AN FRA ORIC (A)	LECUI NTI-S AGMEN SINAI	LOGY LAR SENSE T TY L SOU	TYPE:	E: Ot		nucl	leic	acio	i					
4 5		(v:\	(C) (D) (E) (F) (G)	DEVE TISS CELI CELI	VIDU LOPN SUE T TYP	ENTA YPE: E: IE:	L ST										
EA		(AT)	TUL	TEDIA	ATE S	OURC	: تا.										

```
(A) LIBRARY
                     (B) CLONE:
                 (vii) FEATURE
                     (D) OTHER INFORMATION: sense primer 5
5
                 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:48
            GCTCTAGACTACAGGACTGAGAAGAAGT 28
             (2) INFORMATION FOR SEQ ID NO: 49
10
                 (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 28 bases
                     (B) Type: nucleic acid
                     (C) STRANDNESS: single
                     (D) TOPOLOGY: linear
                 (ii) MOLECUILAR TYPE: Other nucleic acid
15
                 (iii) ANTI-SENSE: YES
                 (iv) FRAGMENT TYPE:
                 (v) ORIGINAL SOURCE:
                     (A)
                     (B) STRAIN:
20
                     (C) INDIVIDUAL ISOLATE:
                     (D) DEVELOPMENTAL STAGE:
                     (E) TISSUE TYPE:
                     (F) CELL TYPE:
                     (G) CELL LINE:
                 (vi) IMMEDIATE SOURCE:
                     (A) LIBRARY
                     (B) CLONE:
                 (vii) FEATURE
                     (D) OTHER INFORMATION: anti-sense primer 5
                 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:49
30
            GCTCTAGAACATTCTCGGTGCCTGTAAC 28
            (2) INFORMATION FOR SEQ ID NO:50
                 (i) SEQUENCE CHARACTERISTICS:
35
                     (A) LENGTH: 28 bases
                     (B) Type: nucleic acid
                    · (C) STRANDNESS: single
                     (D) TOPOLOGY: linear
                 (ii) MOLECUILAR TYPE: Other nucleic acid
                 (iii) ANTI-SENSE: NO
40
                 (iv) FRAGMENT TYPE:
                 (v) ORIGINAL SOURCE:
                     (A)
                     (B) STRAIN:
                     (C) INDIVIDUAL ISOLATE:
                     (D) DEVELOPMENTAL STAGE:
                     (E) TISSUE TYPE:
                     (F) CELL TYPE:
                     (G) CELL LINE:
                 (vi) IMMEDIATE SOURCE:
                     (A) LIBRARY
50
                     (B) CLONE:
                 (vii) FEATURE
```

```
(D) OTHER INFORMATION: sense primer 6
                  (ix) SEQUENCE DESCRIPTION: SEQ ID NO:50
5
             GCTCTAGAGAGAAGGAAACCCTTTCCTG 28
             (2) INFORMATION FOR SEQ ID NO:51
                 (i) SEQUENCE CHARACTERISTICS:
                      (A) LENGTH: 28 bases
10
                      (B) Type: nucleic acid
                      (C) STRANDNESS: single
                      (D) TOPOLOGY: linear
                  (ii) MOLECUILAR TYPE: Other nucleic acid
                 (iii) ANTI-SENSE: YES
15
                 (iv) FRAGMENT TYPE:
                 (v) ORIGINAL SOURCE:
                      (A)
                      (B) STRAIN:
                      (C) INDIVIDUAL ISOLATE:
                      (D) DEVELOPMENTAL STAGE:
20
                      (E) TISSUE TYPE:
                      (F) CELL TYPE:
                     (G) CELL LINE:
                  (vi) IMMEDIATE SOURCE:
                      (A) LIBRARY
                      (B) CLONE:
25
                 (vii) FEATURE
                      (D) OTHER INFORMATION: anti-sense primer 6
                  (ix) SEQUENCE DESCRIPTION: SEQ ID NO:51
             GCTCTAGAATATTCCTGGTGCCCATGAT 28
30
             (2) INFORMATION FOR SEQ ID NO:52
                 (i) SEQUENCE CHARACTERISTICS:
                     (A) LENGTH: 11 amino acids
                     (B) Type: amino acid
35
                     (C) STRANDNESS: double
                     (D) TOPOLOGY: linear
                 (ii) MOLECUILAR TYPE: Peptide
                 (iii) ANTI-SENSE: NO
                 (iv) FRAGMENT TYPE:
                 (v) ORIGINAL SOURCE:
40
                     (A)
                     (B) STRAIN:
                     (C) INDIVIDUAL ISOLATE:
                     (D) DEVELOPMENTAL STAGE:
                     (E) TISSUE TYPE:
                     (F) CELL TYPE:
                     (G) CELL LINE:
                 (vi) IMMEDIATE SOURCE:
                     (A) LIBRARY
                     (B) CLONE:
                 (vii) FEATURE
50
                     (D) OTHER INFORMATION: Peptide 1
                 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:52
```

```
Leu Val Met Met Glu Gly Lys Met Met Ser Tyr
       (2) INFORMATION FOR SEQ ID NO:53
5
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 20 amino acids
                (B) Type: amino acid
                (C) STRANDNESS: double
                (D) TOPOLOGY: linear
10
            (ii) MOLECUILAR TYPE: Peptide
            (iii) ANTI-SENSE: NO
            (iv) FRAGMENT TYPE:
            (v) ORIGINAL SOURCE:
                (A)
                (B) STRAIN:
15
                (C) INDIVIDUAL ISOLATE:
                (D) DEVELOPMENTAL STAGE:
                (E) TISSUE TYPE:
                (F) CELL TYPE:
                (G) CELL LINE:
20
            (vi) IMMEDIATE SOURCE:
                (A) LIBRARY
                (B) CLONE:
            (vii) FEATURE
                (D) OTHER INFORMATION: peptide 2
25
            (vii) SEQUENCE DESCRIPTION: SEQ ID NO:53
       Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr
                                            10
       Gly Ile Val Leu Leu
30
       (2) INFORMATION FOR SEQ ID NO:54
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 16 amino acids
35
                (B) Type: amino acids
                (C) STRANDNESS: double
                (D) TOPOLOGY: linear
            (ii) MOLECUILAR TYPE: Peptide
            (iii) ANTI-SENSE: NO
40
            (iv) FRAGMENT TYPE:
            (v) ORIGINAL SOURCE:
                (A)
                (B) STRAIN:
                (C) INDIVIDUAL ISOLATE:
                (D) DEVELOPMENTAL STAGE:
45
                (E) TISSUE TYPE:
                (F) CELL TYPE:
                (G) CELL LINE:
            (vi) IMMEDIATE SOURCE:
                (A) LIBRARY
50
                (B) CLONE:
           (vii) FEATURE
```

(D) OTHER INFORMATION: peptide 3

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:54 Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser (2) INFORMATION FOR SEQ ID NO:55 (i) SEQUENCE CHARACTERISTICS: 10 (A) LENGTH: 13 amino acids (B) Type: amino acid (C) STRANDNESS: (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Peptide (iii) ANTI-SENSE: NO 15 (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE:
(D) DEVELOPMENTAL STAGE: 20 (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY 25 (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: peptide 4 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:55 30 Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe 5 10 (2) INFORMATION FOR SEQ ID NO:56 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 bases 35 (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO 40 (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: 45 (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE

	(D) OTHER INFORMATION: sense primer 7 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:56
5	CACCTGCAGAAGGAGCTGGCAGAA 24
10	(2) INFORMATION FOR SEQ ID NO:57 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid
15	<pre>(iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE:</pre>
20	(C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE:
25	 (A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: anti-sense primer 7 (ix) SEQUENCE DESCRIPTION: SEQ ID NO: 57
30	AATAAGCTTGGTACCCTATTAGAGCTTATATAA 33 (2) INFORMATION FOR SEQ ID NO:58 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 bases
35	(B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO
40	<pre>(iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE:</pre>
45	(D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY
50	(B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: sense primer 8 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:58

TGCGAATTCACCATGCTGGGCATCTGG (2) INFORMATION FOR SEQ ID NO:59 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 36 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid 10 (iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: 15 (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: 20 (A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: anti-sense primer 8 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:59 25 AACCTGCAGGTGGAAGAGCTGAGCAACAGACGTAAG (2) INFORMATION FOR SEQ ID NO:60 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 30 (B) Type: nucleic acid (C) STRANDNESS: (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO 35 (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: 40 (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY 45 (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: human Fas ligand (ix) SEQUENCE DESCRIPTION: SEQ ID NO:60 Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His

...

	(2)	<pre>INFORMATION FOR SEQ ID NO:61 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 bases</pre>
5		(B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear
	•	(ii) MOLECUILAR TYPE: Other nucleic acid
		(iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE:
10		(v) ORIGINAL SOURCE: (A)
		(B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE:
15		(E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE:
		<pre>(vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE:</pre>
20		(vii) FEATURE (D) OTHER INFORMATION: PS type S20
		(ix) SEQUENCE DESCRIPTION: SEQ ID NO:61
25	TAA	AACCGTTTGCTGGGGCTGG 22
	(2)	INFORMATION FOR SEQ ID NO:62 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 bases (B) Type: nucleic acid
30		(C) STRANDNESS: double (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid
35		(iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE:
	,	(A)(B) STRAIN:(C) INDIVIDUAL ISOLATE:(D) DEVELOPMENTAL STAGE:(E) TISSUE TYPE:
40	-	(E) TISSUE TIPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE:
		(A) LIBRARY (B) CLONE:
45		(vii) FEATURE (D) OTHER INFORMATION: PS type A41 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:62
,	CCAC	GCCCCAGCAAACGGTTTTA 22
50	(2)	INFORMATION FOR SEQ ID NO:63 (i) SEQUENCE CHARACTERISTICS:

5	 (A) LENGTH: 20 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE:
	(A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE:
15	(G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE
20	(D) OTHER INFORMATION: PS type S50 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:63
	ACCAGCTGCCATGCAGCAGC 20
25	<pre>(2) INFORMATION FOR SEQ ID NO:64 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) Type: nucleic acid (C) STRANDNESS: single</pre>
30	 (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE:
35	(A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE:
40	(G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE
	(D) OTHER INFORMATION: PS type A69 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:64 GCTGCTGCATGGCAGCTGGT 20
50	(2) INFORMATION FOR SEQ ID NO:65 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 bases (B) Type: nucleic acid (C) STRANDNESS: single

5	 (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A)
10	(B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE:
15	<pre>(vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: PS type S163 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:65</pre>
20	CTGTGCCCAGAAGGCCTGGTCA 22
	(2) INFORMATION FOR SEQ ID NO:66 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 bases (B) Type: nucleic acid (C) STRANDNESS: single
25	 (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE:
30	<pre>(vii) FEATURE (D) OTHER INFORMATION: PS type A184 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:66</pre>
	TGACCAGGCCTTCTGGGCACAG 22
35	(2) INFORMATION FOR SEQ ID NO:67 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 bases (B) Type: nucleic acid
40	<pre>(C) STRANDNESS: double (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE:</pre>
45	(VII) FEATURE (D) OTHER INFORMATION: PS type S338 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:67
	CTTGGTAGGATTGGGCCT 18
50	(2) INFORMATION FOR SEQ ID NO:68 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 bases (B) Type: nucleic acid

5	(C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A)
10	(B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE:
15	(A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: PS type A355 (vii) SEQUENCE DESCRIPTION: SEQ ID NO:68
20	AGGCCCAATCCTACCAAG 18
	(2) INFORMATION FOR SEQ ID NO:69 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 bases (B) Type: nucleic acid
25	<pre>(C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE:</pre>
30	<pre>(v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE:</pre>
35	(E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY
40	(B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: PS type S484 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:69
	AGCTGAGGAAAGTGGCCCATTT 22
45	(2) INFORMATION FOR SEQ ID NO:70 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 bases (B) Type: nucleic acid (C) STRANDNESS: single
50	(D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid

5	(iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE:
10	(E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (Vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE:
15	(vii) FEATURE (D) OTHER INFORMATION: PS type A505 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:70
	AAATGGGCCACTTTCCTCAGCT 22
20	(2) INFORMATION FOR SEQ ID NO:71 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) Type: nucleic acid
25	<pre>(C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE:</pre>
30	(V) ORIGINAL SOURCE: (A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE:
35	<pre>(F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE:</pre>
40	(vii) FEATURE (D) OTHER INFORMATION: PS tupe S714 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:71 CCCCAGGATCTGGTGATGAT 20
45	(2) INFORMATION FOR SEQ ID NO:72 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) Type: nucleic acid (C) STRANDNESS: single
50	 (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE:

5	(A) (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (VI) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (VII) FEATURE- (D) OTHER INFORMATION: PS type A733 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:72
15 P	ATCATCACCAGATCCTGGGG 20
20	(2) INFORMATION FOR SEQ ID NO:73 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO
25	(iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) (B) STRAIN:
30	(C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (VI) IMMEDIATE SOURCE:
35	(A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: PS type S905 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:73
40	AGAGAAGCACTTTGGGATTC 20 (2) INFORMATION FOR SEQ ID NO:74 (1) SEQUENCE CHARACTERISTICS:
45	(A) LENGTH: 20 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE:
50 .	(A) (B) STRAIN: (C) INDIVIDUAL ISOLATE:

```
(D) DEVELOPMENTAL STAGE:
                 (E) TISSUE TYPE:
                 (F) CELL TYPE:
                 (G) CELL LINE:
5
             (vi) IMMEDIATE SOURCE:
                 (A) LIBRARY
                 (B) CLONE:
             (vii) FEATURE
                 (D) OTHER INFORMATION
10
                       : PS type anti-sense oligonucleotide A924
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74
        GAATCCCAAAGTGCTTCTCT 20
         (2) INFORMATION FOR SEQ ID NO:75
15
             SKIPPED
        (2) INFORMATION FOR SEQ ID NO:76
             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 141 amino acids
20
                 (B) Type: nucleic acid
                 (C) STRANDNESS: double
                 (D) TOPOLOGY: linear
             (ii) MOLECUILAR TYPE: amino acid
             (iii) ANTI-SENSE: NO
25
             (iv) FRAGMENT TYPE:
             (v) ORIGINAL SOURCE:
                 (A) human
                 (B) STRAIN:
                 (C) INDIVIDUAL ISOLATE:
30
                 (D) DEVELOPMENTAL STAGE:
                 (E) TISSUE TYPE:
                 (F) CELL TYPE:
                 (G) CELL LINE:
             (vi) IMMEDIATE SOURCE:
                 (A) LIBRARY
                 (B) CLONE:
             (vii) FEATURE
                  (D) OTHER INFORMATION: Polypeptide ND38
             (ix) SEQUENCE DESCRIPTION: SEQ ID NO:76
40
        Lys Glu Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser
          1
                                                                   . 15
                                               10
        Arg Ser Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu
        Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu
45
                          35
                                               40
        Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln
                          50
                                              55
        Ser Cys Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn
                          65
        Ser Lys Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met
50
                          80
                                              85
        Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu
```

```
95
                                              100
        Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn
                         110
                                              115
        Val Ser Glu Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe
                         125
                                              130
        Phe Gly Leu Tyr Lys Leu
                         140 141
        (2) INFORMATION FOR SEQ ID NO:77
10
             (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 139 amino acids
                 (B) Type: nucleic acid
                 (C) STRANDNESS: double
                 (D) TOPOLOGY: linear
             (ii) MOLECUILAR TYPE: amino acid
15
           (iii) ANTI-SENSE: NO
             (iv) FRAGMENT TYPE:
             (v) ORIGINAL SOURCE:
                 (A) human
                 (B) STRAIN:
20
                 (C) INDIVIDUAL ISOLATE:
                 (D) DEVELOPMENTAL STAGE:
                 (E) TISSUE TYPE:
                 (F) CELL TYPE:
                 (G) CELL LINE:
25
            (vi) IMMEDIATE SOURCE:
                 (A) LIBRARY
                 (B) CLONE:
            (vii) FEATURE
                 (D) OTHER INFORMATION: Polypeptide ND40
            (ix) SEQUENCE DESCRIPTION: SEQ ID NO:77
30
        Leu Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser
                                                                   15
        Met Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser
                          20
                                                                   30
35
        Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly
                          35
                                               40
        Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys
                          50
                                              55
        Asn Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys
                          65
40
        Tyr Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr
                          80
                                              85
                                                                   90
        Cys Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala
                          95
                                             100
        Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser
45
                         110
                                             115
                                                                  120
        Glu Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly
                         125
                                             130
                                                                  135
        Leu Tyr Lys Leu
                    139
50
        (2) INFORMATION FOR SEQ ID NO:78
            (i) SEQUENCE CHARACTERISTICS:
```

```
(A) LENGTH: 138 amino acids
                (B) Type: amino acid
                (C) STRANDNESS:
                (D) TOPOLOGY: linear
            (ii) MOLECUILAR TYPE: Polypeptide
            (iii) ANTI-SENSE: NO
            (iv) FRAGMENT TYPE:
            (v) ORIGINAL SOURCE:
                (A) human
10
                (B) STRAIN:
                (C) INDIVIDUAL ISOLATE:
                (D) DEVELOPMENTAL STAGE:
                (E) TISSUE TYPE:
                (F) CELL TYPE:
                (G) CELL LINE:
15
            (vi) IMMEDIATE SOURCE:
                (A) LIBRARY
                (B) CLONE:
            (vii) FEATURE
                (D) OTHER INFORMATION: polypeptide ND41
20
            (ix) SEQUENCE DESCRIPTION: SEQ ID NO:78
        Arg Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met
                                              10
                                                                   15
       Pro Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly
25
                         20
                                              25
       Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu
                                              40
                                                                   45
       Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn
                         50
                                                                   60
       Asn Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr
30
                         65
                                                                   75
                                              70
       Pro Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys
                         80
                                              85
       Thr Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val
                         95
                                             100
35
       Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu
                        110
                                             115
                                                                  120
       Leu Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu
                        125
       Tyr Lys Leu
               138
40
       (2) INFORMATION FOR SEQ ID NO:79
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 137 amino acids
                (B) Type: nucleic acid
45
                (C) STRANDNESS:
                (D) TOPOLOGY: linear
            (ii) MOLECUILAR TYPE: Polypeptide
            (iii) ANTI-SENSE: NO
            (iv) FRAGMENT TYPE:
            (v) ORIGINAL SOURCE:
50
                (A) human
                (B) STRAIN:
```

```
(C) INDIVIDUAL ISOLATE:
                (D) DEVELOPMENTAL STAGE:
                (E) TISSUE TYPE:
                (F) CELL TYPE:
                (G) CELL LINE:
            (vi) IMMEDIATE SOURCE:
                (A) LIBRARY
                (B) CLONE:
            (vii) FEATURE
                (D) OTHER INFORMATION: Polypeptide ND42
10
            (ix) SEQUENCE DESCRIPTION: SEQ ID NO:79
       Lys Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro
                                              10
                                                                 15
       Leu Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val
15
                         20
                                              25
       Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr
                                              40
                                                                   45
       Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn
                         50
20
       Leu Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro
                         65
                                              70
                                                                   75
       Gln Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr
                         80
                                              85
       Thr Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe
                         95
                                             100
25
       Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu
                        110
                                             115
                                                                  120
       Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr
                        125
                                             130
       Lys Leu
30
           137
       (2) INFORMATION FOR SEQ ID NO:80
           (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 136 amino acids
35
                (B) Type: nucleic acid
                (C) STRANDNESS: double
                (D) TOPOLOGY: linear
           (ii) MOLECUILAR TYPE: Polypeptide
           (iii) ANTI-SENSE: NO
           (iv) FRAGMENT TYPE:
40
           (v) ORIGINAL SOURCE:
                (A) human
                (B) STRAIN:
                (C) INDIVIDUAL ISOLATE:
                (D) DEVELOPMENTAL STAGE:
45
               (E) TISSUE TYPE:
                (F) CELL TYPE:
               (G) CELL LINE:
           (vi) IMMEDIATE SOURCE:
               (A) LIBRARY
               (B) CLONE:
50
           (vii) FEATURE
               (D) OTHER INFORMATION: polypeptide ND43
```

(ix) SEQUENCE DESCRIPTION: SEQ ID NO:80 Val Ala His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu 10 15 5 Glu Trp Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys 25 20 30 Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu 10 55 60 50 Pro Leu Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln 65 70 75 Asp Leu Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr 80 85 Gly Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn 15 95 100 105 Leu Thr Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser 110 115 120 Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys 125 130 135 20 Leu 136 (2) INFORMATION FOR SEQ ID NO:81 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 178 amino acids 25 (B) Type: nucleic acid (C) STRANDNESS: (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: polypeptide (iii) ANTI-SENSE: NO 30 (iv) FRAGMENT TYPE: (v) ORIGINAL SOURCE: (A) human (B) STRAIN: (C) INDIVIDUAL ISOLATE: 35 (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY 40 (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: polypeptide CD179 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:81 45 Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu Ser 10 15 Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu Lys Gln Ile Gly 20 25 30 His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala 35 40 45 50 His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp

55

55

```
Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys
                                               70
        Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
                          80
                                               85
                                                                    90
        Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu
                          95
                                              100
        Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu
                         110
                                              115
                                                                  120
        Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln
10
                         125
                                              130
                                                                   135
        Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr
                         140
                                              145
        Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val
                         155
                                              160
        Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys
15
                         170
                                             175
                                                          178
        (2) INFORMATION FOR SEQ ID NO:82
            (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 45 bases
20
                (B) Type: nucleic acid
                 (C) STRANDNESS: single
                (D) TOPOLOGY: linear
            (ii) MOLECUILAR TYPE: Other nucleic acid
            (iii) ANTI-SENSE: YES
            (iv) FRAGMENT TYPE: internal fragment
25
            (v) ORIGINAL SOURCE:
                 (A) human
                (B) STRAIN:
                (C) INDIVIDUAL ISOLATE:
                (D) DEVELOPMENTAL STAGE:
30
                 (E) TISSUE TYPE:
                (F) CELL TYPE:
                 (G) CELL LINE:
            (vi) IMMEDIATE SOURCE:
                (A) LIBRARY
35
                (B) CLONE:
            (vii) FEATURE
                (D) OTHER INFORMATION: anti-sense oligonucleotide 9
            (ix) SEQUENCE DESCRIPTION: SEQ ID NO:82
        CTTCTGCAGGTGGAAGAGCTGAGCGACACTAGTCAGAACCAGAGG
40
        (2) INFORMATION FOR SEQ ID NO:83
            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 45 bases
                (B) Type: nucleic acid
45
                (C) STRANDNESS: single
                (D) TOPOLOGY: linear
            (ii) MOLECUILAR TYPE: Other nucleic acid
            (iii) ANTI-SENSE: NO
            (iv) FRAGMENT TYPE: internal fragment
            (v) ORIGINAL SOURCE:
50
                (A) human
                (B) STRAIN:
```

```
(C) INDIVIDUAL ISOLATE:
                 (D) DEVELOPMENTAL STAGE:
                 (E) TISSUE TYPE:
                 (F) CELL TYPE:
                 (G) CELL LINE:
            (vi) IMMEDIATE SOURCE:
                 (A) LIBRARY
                 (B) CLONE:
            (vii) FEATURE
10
                 (D) OTHER INFORMATION: sense oligonucleotide 9
            (ix) SEQUENCE DESCRIPTION: SEQ ID NO:83
        AATTCACCATGCTGGGCATCTGGACCCTCCTACCTCTGGTTCTGA 45
        (2) INFORMATION FOR SEQ ID NO:84
15
            (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 45 bases
                 (B) Type: nucleic acid
                 (C) STRANDNESS: single
                 (D) TOPOLOGY: linear
20
            (ii) MOLECUILAR TYPE: Other nucleic acid
            (iii) ANTI-SENSE: YES
            (iv) FRAGMENT TYPE: internal fragment
            (v) ORIGINAL SOURCE:
                (A) human
                (B) STRAIN:
25
                (C) INDIVIDUAL ISOLATE:
                (D) DEVELOPMENTAL STAGE:
                (E) TISSUE TYPE:
                (F) CELL TYPE:
                (G) CELL LINE:
            (vi) IMMEDIATE SOURCE:
                (A) LIBRARY
                (B) CLONE:
            (vii) FEATURE
                (D) OTHER INFORMATION: anti-sense oligonucleotide 10
            (ix) SEQUENCE DESCRIPTION: SEQ ID NO:84
35
        CTAGTCAGAACCAGAGGTAGGAGGGTCCAGATGCCCAGCATGGTG 45
        (2) INFORMATION FOR SEQ ID NO:85
            (i) SEQUENCE CHARACTERISTICS:
40
                (A) LENGTH: 30 bases
                (B) Type: nucleic acid(C) STRANDNESS: single
                (D) TOPOLOGY: linear
            (ii) MOLECUILAR TYPE: Other nucleic acid
45
            (iii) ANTI-SENSE: NO
            (iv) FRAGMENT TYPE: internal fragment
            (v) ORIGINAL SOURCE:
                (A) human
                (B) STRAIN:(C) INDIVIDUAL ISOLATE:
50
                (D) DEVELOPMENTAL STAGE:
              . (E) TISSUE TYPE:
```

	}
	(F) CELL TYPE:
	(G) CELL LINE:
	(vi) IMMEDIATE SOURCE:
	(A) LIBRARY
5	(B) CLONE:
	(vii) FEATURE
	(D) OTHER INFORMATION: sense primer 11
	(ix) SEQUENCE DESCRIPTION: SEQ ID NO:85
10	CTGACTAGTGTCGCTAAGGAGCTGAGGAAA 30
	(2) INFORMATION FOR SEQ ID NO:86
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 20 bases
15	(B) Type: nucleic acid
•	(C) STRANDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECUILAR TYPE: Other nucleic acid
•	(iii) ANTI-SENSE: YES
	(iv) FRAGMENT TYPE: internal fragment
20	(v) ORIGINAL SOURCE:
	(A) human
	(B) STRAIN: (C) INDIVIDUAL ISOLATE:
	(C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE:
	(E) TISSUE TYPE:
25	(F) CELL TYPE:
	(G) CELL LINE:
	(vi) IMMEDIATE SOURCE:
	(A) LIBRARY
,	(B) CLONE:
30	(vii) FEATURE
	(D) OTHER INFORMATION: anti-sense primer 11
•	(ix) SEQUENCE DESCRIPTION: SEQ ID NO:86
	, , , , , , , , , , , , , , , , , , ,
	TAAGCCGAAAAACGTCTGAG 20
35	
	(2) INFORMATION FOR SEQ ID NO:87
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 30 bases
	(B) Type: nucleic acid
40	(C) STRANDNESS: single
	(D) TOPOLOGY: linear
	(ii) MOLECUILAR TYPE: Other nucleic acid
	(iii) ANTI-SENSE: NO
	(iv) FRAGMENT TYPE: internal fragment
45	(v) ORIGINAL SOURCE:
45	(A) human
	(B) STRAIN: (C) INDIVIDUAL ISOLATE:
	(D) DEVELOPMENTAL STAGE:
	(E) TISSUE TYPE:
	(F) CELL TYPE:
50	(G) CELL LINE:
	(vi) IMMEDIATE SOURCE:
	11 Transporter Coordan

5	(A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: sense primer 12 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:87
	CTGACTAGTGTCGCTCTGAGGAAAGTGGCC 30
10	(2) INFORMATION FOR SEQ ID NO:88 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) Type: nucleic acid (C) STRANDNESS: single
15	(D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE: internal fragment
20	(v) ORIGINAL SOURCE: (A) human (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE:
25	(F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE
30	(D) OTHER INFORMATION: sense primer 13 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:88 CTGACTAGTGTCGCTAGGAAAGTGGCCCAT 30
35	(2) INFORMATION FOR SEQ ID NO:89 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear
40	(ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE: internal fragment (v) ORIGINAL SOURCE: (A) human
45	(B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE:
50	(G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE

	(D) OTHER INFORMATION: sense primer 14 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:89
5	CTGACTAGTGTCGCTAAAGTGGCCCATTTA 30
10	(2) INFORMATION FOR SEQ ID NO:90 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 30 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid
15	(iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE: internal fragment (v) ORIGINAL SOURCE: (A) human (B) STRAIN:
20	(C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (VI) IMMEDIATE SOURCE:
25	(A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: sense primer 15 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:90
30	CTGACTAGTGTCGCTGTGGCCCATTTAACA 30 (2) INFORMATION FOR SEQ ID NO:91 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 bases
35	 (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: YES
40	<pre>(iv) FRAGMENT TYPE: internal fragment (v) ORIGINAL SOURCE: (A) human (B) STRAIN: (C) INDIVIDUAL ISOLATE:</pre>
45	(D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY
50	(B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: anti-sense primer 16 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:91

CTTGGTACCCTATTACTTATATAAGCC 27 (2) INFORMATION FOR SEQ ID NO:92 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid 10 (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE: internal fragment (v) ORIGINAL SOURCE: (A) human (B) STRAIN: (C) INDIVIDUAL ISOLATE: 15 (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE: (vi) IMMEDIATE SOURCE: 20 (A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: sense primer 16 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:92 25 GAGCTACTGCACTACTGGGC 20 (2) INFORMATION FOR SEQ ID NO:93 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 39 bases 30 (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: YES 35 (iv) FRAGMENT TYPE: internal fragment (v) ORIGINAL SOURCE: (A) human (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: 40 (E) TISSUE TYPE (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE 45 (D) OTHER INFORMATION: anti-sense primer 17 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:93 CGCGGATCCGGTACCTTTTTTGGTAACCGGGGTAAACAG 39 (2) INFORMATION FOR SEQ ID NO:94 50 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 bases

5	(B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear (ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE: internal fragment (v) ORIGINAL SOURCE: (A) human
10	(B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE:
15	(G) CELL LINE: (vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: sense primer 17
20	(ix) SEQUENCE DESCRIPTION: SEQ ID NO:94 CGCAAGTTCACGTAAAAAGC 20
25	(2) INFORMATION FOR SEQ ID NO:95 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear
30	<pre>(ii) MOLECUILAR TYPE: Other nucleic acid (iii) ANTI-SENSE: NO (iv) FRAGMENT TYPE: internal fragment (v) ORIGINAL SOURCE: (A) human</pre>
35	(A) Identify (B) STRAIN: (C) INDIVIDUAL ISOLATE: (D) DEVELOPMENTAL STAGE: (E) TISSUE TYPE: (F) CELL TYPE: (G) CELL LINE:
40	(vi) IMMEDIATE SOURCE: (A) LIBRARY (B) CLONE: (vii) FEATURE (D) OTHER INFORMATION: sense primer 18 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:95
45	TTGAAGCTTAAAAAAGGGTATAAAATAAAATGCAGCTCTTCCACCT 46
50	(2) INFORMATION FOR SEQ ID NO:96 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 bases (B) Type: nucleic acid (C) STRANDNESS: single (D) TOPOLOGY: linear

	(ii) MOLECUILAR TYPE: Other nucleic acid
	(iii) ANTI-SENSE: YES
	(iv) FRAGMENT TYPE: internal fragment
	(v) ORIGINAL SOURCE:
5	(A) human
	(B) STRAIN:
	(C) INDIVIDUAL ISOLATE:
	(D) DEVELOPMENTAL STAGE:
	(E) TISSUE TYPE:
10	(F) CELL TYPE:
	(G) CELL LINE:
	(vi) IMMEDIATE SOURCE:
	(A) LIBRARY
	(B) CLONE:
	(vii) FEATURE
15	(D) OTHER INFORMATION: anti-sense primer 18
	(ix) SEQUENCE DESCRIPTION: SEQ ID NO:96
	AAGGTCGACTATTAGAGCTTATATAAGCC 29
•	
20	(2) INFORMATION FOR SEQ ID NO:97
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 30 bases
	(B) Type: nucleic acid
	(C) STRANDNESS: single
	(D) TOPOLOGY: linear
25	(ii) MOLECUILAR TYPE: Other nucleic acid
	(iii) ANTI-SENSE: NO
	(iv) FRAGMENT TYPE: internal fragment
	(v) ORIGINAL SOURCE:
	(A) human
	(B) STRAIN:
30	
	(C) INDIVIDUAL ISOLATE:
	(D) DEVELOPMENTAL STAGE:
	(vi) IMMEDIATE SOURCE:
	(A) LIBRARY
	(B) CLONE:
35 .	(vii) FEATURE
	(D) OTHER INFORMATION: sense primer 19
	(ix) SEQUENCE DESCRIPTION: SEQ ID NO:97
	GGGGGTTACCAAAGCCCAGCTCTTCCACCT 30
40	
	(2) INFORMATION FOR SEQ ID NO:98
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 25 bases
	(B) Type: nucleic acid
	(C) STRANDNESS: single
45	(D) TOPOLOGY: linear
	(ii) MOLECUILAR TYPE: Other nucleic acid
	(iii) ANTI-SENSE: NO
	(iv) FRAGMENT TYPE: internal fragment
	(v) ORIGINAL SOURCE:
50	(A) human
	(B) STRAIN:

	(C) INDIVIDUAL ISOLATE:
	(D) DEVELOPMENTAL STAGE:
	(E) TISSUE TYPE:
5	(F) CELL TYPE:
	(G) CELL LINE:
	(vi) IMMEDIATE SOURCE: (A) LIBRARY
	(B) CLONE:
	(vii) FEATURE
10	(D) OTHER INFORMATION: sense primer 20
	(ix) SEQUENCE DESCRIPTION: SEQ ID NO:98
	(au)
	CCCGGTTACCAAAGCCAAGGAGCTG 25
15	(2) INFORMATION FOR SEQ ID NO:99
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 20 base
	(B) Type: nucleic acid
	(C) STRANDNESS: single
20	(D) TOPOLOGY: linear
	(ii) MOLECUILAR TYPE: Other nucleic acid
	<pre>(iii) ANTI-SENSE: YES (iv) FRAGMENT TYPE: internal fragment</pre>
	(v) ORIGINAL SOURCE:
	(A) human
25	(B) STRAIN:
	(C) INDIVIDUAL ISOLATE:
	(D) DEVELOPMENTAL STAGE:
	(E) TISSUE TYPE:
	(F) CELL TYPE:
30	(G) CELL LINE:
	(vi) IMMEDIATE SOURCE:
•	(A) LIBRARY
	(B) CLONE:
	<pre>(viii) FEATURE: (D) OTHER INFORMATION: anti-sense primer 20</pre>
35	(ix) SEQUENCE DESCRIPTION: SEQ ID NO:99
	TAAGCCGAAAAACGTCTGAG 20
	(2) INFORMATION FOR SEQ ID NO:100
40	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 927 base
	(B) Type: nucleic acid
	(C) STRANDNESS: double (D) TOPOLOGY: linear
	(ii) MOLECUILAR TYPE: Other nucleic acid
45	(iii) ANTI-SENSE: YES OR NO
	(V) ORIGINAL SOURCE:
	(A) mouse(gld)
	(C) INDIVIDUAL ISOLATE:
	(D) DEVELOPMENTAL STAGE: rearrenged
50	(E) TISSUE TYPE:
	(vi) IMMEDIATE SOURCE:
	(A) LIBRARY

(B) CLONE: (vii) SEQUENCE DESCRIPTION: SEQ ID NO:100

5.							GAG	AAGG.	A AA	CCCT	TTCC	TGG	GGCT	GG G	TGCC	32
	ATG	CAG	CAG	ccc	ATG	AAT	TAC	CCA	TGT	ccc	CAG	ATC	TTC	TGG	GTA	77
	GAC	AGC	AGT	GCC	ACT	TÇA	TCT	TGG	GCT	CCT	CCA	GGG	TCA	GTT	TTT	122
10	ccc	TGT	CCA	TCT	TGT	GGG	CCT	AGA	GGG	CCG	GAC	CAA	AGG	AGA	CCG	167
	CCA	CCT	CCA	CCA	CCA	CCT	GTG	TCA	CCA	CTA	CCA	CCG	CCA	TCA	CAA	212
	CCA	CTC	CCA	CTG	CCG	CCA	CTG	ACC	ССТ	СТА	AAG	AAG	AAG	GAC	CAC	257
15	AAC	ACA	AAT	CTG	TGG	CTA	CCG	GTG	GTA	TTT	TTC	ATG	GTT	CTG	GTG	302
	GCT	CTG	GTT	GGA	ATG	GGA	TTA	GGA	ATG	TAT	CAG	CTC	TTC	CAC	CTG	347
20	CAG	AAG	GAA	CTG	GCA	GAA	CTC	CGT	GAG	TTC	ACC	AAC	CAA	AGC	CTT	392
	AAA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	ATA	GCC	AAC	ccc	AGT	ACA	ССС	437
	TCT	GAA	AAA	AAA	GAG	CCG	AGG	AGT	GTG	GCC	CAT	TTA	ACA	GGG	AAC	482
25	ccc	CAC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	527
	ACC	GCT	CTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	AAA	GGT	GGC	CTT	GTG	572
30	ATC	AAC	GAA	ACT	GGG	TTG	TAC	TTC	GTG	TAT	TCC	AAA	GTA	TAC	TTC	617
	CGG	GGT	CAG	TCT	TGC	AAC	AAC	CAG	ccc	CTA	AAC	CAC	AAG	GTC	TAT	662
	ATG	AGG	AAC	TCT	AAG	TAT	ССТ	GAG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	707
35	AAG	AGG	TTG	AAC	TAC	TGC	ACT	ACT	GGA	CAG	ATA	TGG	GCC	CAC	AGC	752
	AGC	TAC	CTG	GGG	GCA	GTA	TTC	AAT	CTT	ACC	AGT	GCT	GAC	CAT	TTA	797
	TAT	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	842
40	AAG	ACC	CTT	TTC	GGC	TTG	TAT	AAG	CTT	TAA	AAGA	AAAA	GCAI	TTT?	AAAT	892
	GATO	TACI	TAT I	CTTT	ATCA	T GG	GCAC	CAGG	AA1	TAT	•					927

Claims

 A polypeptide comprising an amino acid sequence represented by the following formula 1 (SEQ ID NO: 1):

55

formula 1

5	Lys 1	Val	Ala	His	Leu 5	Thr	Gly	Lys	Ser	Asn 10	Ser	Arg	Ser	Met	Pro 15
	Leu	Glu	Trp	Glu	Asp 20	Thr	Tyr	Gly	Ile	Val 25	Leu	Leu	Ser	Gly	Val 30
	Lys	Tyr	Lys	Lys	Gly 35	Gly	Leu	Val	Ile	Asn 40	Glu	Thr	Gly	Leu	Tyr 45
10	Phe	Val	Tyr	Ser	Lys 50	Val	Tyr	Phe	Arg	Gly 55	Gln	Ser	Суѕ	Asn	Asn 60
	Leu	Pro	Leu	Ser	His 65	Lys	Val	Tyr	Met	Arg 70	Asn	Ser	Lys	Tyr	Pro 75
15	Gln	Asp	Leu	Val	Met 80	Met	Glu	Gly	Lys	Met 85	Met	Ser	Tyr	Cys	Thr 90
	Thr	Gly	Gln	Met	Trp 95	Ala	Arg	Ser	Ser	Tyr 100	Leu	Gly	Ala	Val	Phe 105
	Asn	Leu	Thr	Ser	Ala 110	Asp	His	Leu	Tyr	Val 115	Asn	Val	Ser	Glu	Leu 120
20	Ser	Leu	Val	Asn	Phe 125	Glu	Glu	Ser	Gln	Thr 130	Phe	Phe	Gly	Leu	Tyr 135
	Lys	Leu 137													

25

- A polypeptide comprising an amino acid sequence represented by the following formula 2 (SEQ ID NO: 2):
- 30 formula 2

A polypeptide comprising an amino acid sequence represented by the following formula 3 (SEQ ID NO:
 3):

```
formula 3
5
     Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu Ser
     Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu Lys Gln Ile Gly
                                           25
                                                                30
10
     His Pro Ser Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala
     His Leu Thr Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp
                      50
                                                                60
     Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys
                      65
     Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr
                                                                90
     Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu
20
     Ser His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu
                                                               120
                     110
                                          115
     Val Met Met Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln
                     125
                                          130
     Met Trp Ala Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr
25
                     140
                                          145
                                                               150
     Ser Ala Asp His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val
                     155
                                          160
     Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
30
```

 A polypeptide comprising an amino acid sequence represented by the following formula 4 (SEQ ID NO: 4):

formula 4

Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val

1 5 10 15

Asp Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu
20 25 30

Pro Cys Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro

50

45

35

```
35
    Pro Pro Pro Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro
                      50
                                           55
     Pro Pro Leu Pro Pro Leu Pro Leu Pro Leu Lys Lys Arg Gly
                                           70
     Asn His Ser Thr Gly Leu Cys Leu Leu Val Met Phe Phe Met Val
                      80
                                           85
                                                                90
     Leu Val Ala Leu Val Gly Leu Gly Leu Gly Met Phe Gln Leu Phe
                      95
                                          100
10
     His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu Ser Thr Ser Gln
                     110
                                          115
    Met His Thr Ala Ser Ser Leu Glu Lys Gln Ile Gly His Pro Ser
                     125
                                          130
    Pro Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr
15
                     140
                                          145
    Gly Lys Ser Asn Ser Arg Ser Met Pro Leu Glu Trp Glu Asp Thr
                                          160
    Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly
                     170
                                          175
20
    Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val
                     185
                                          190
     Tyr Phe Arg Gly Gln Ser Cys Asn Asn Leu Pro Leu Ser His Lys
                     200
                                          205
    Val Tyr Met Arg Asn Ser Lys Tyr Pro Gln Asp Leu Val Met Met
25
                     215
                                          220
    Glu Gly Lys Met Met Ser Tyr Cys Thr Thr Gly Gln Met Trp Ala
                     230
                                          235
    Arg Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp
                     245
                                          250
                                                               255
30
    His Leu Tyr Val Asn Val Ser Glu Leu Ser Leu Val Asn Phe Glu
                     260
                                          265
                                                               270
    Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu
                     275
                                          280 281
```

- 5. A polypeptide comprising an amino acid sequence represented by the following formula 5 (SEQ ID NO:
- formula 5

```
Ser Val Ala His Leu Thr Gly Asn Pro Arg Ser Arg Ser Ile Pro
     Leu Glu Trp Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val
45
                                                                30
                                           25
     Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Ala Gly Leu Tyr
                                           40
     Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Ser
                      50
                                                                60
50
     Gln Pro Leu Ser His Lys Val Tyr Met Arg Asn Phe Lys Tyr Pro
                      65
                                           70
     Gly Asp Leu Val Leu Met Glu Glu Lys Lys Leu Asn Tyr Cys Thr
     Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val Phe
```

95 100 105
Asn Leu Thr Val Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu
110 115 120
Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu Tyr
125 130 135
Lys Leu
137

A polypeptide comprising an amino acid sequence represented by the following formula 6 (SEQ ID NO:
 6):

15 formula 6

Arg Ser Val Ala His Leu Thr Gly Asn Pro Arg Ser Arg Ser Ile Pro Leu Glu Trp Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Ala Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Ser Gln Pro Leu Ser His Lys Val Tyr Met Arg Asn Phe Lys Tyr Pro Gly Asp Leu Val Leu Met Glu Glu Lys Lys Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Val Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu Tyr Lys Leu

7. A polypeptide comprising an amino acid sequence represented by the following formula 7 (SEQ ID NO:7):

formula 7

```
Lys Gly Gly Leu Val Ile Asn Glu Ala Gly Leu Tyr Phe Val Tyr
                                           85
    Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Ser Gln Pro Leu
                                          100
                      95
5
    Ser His Lys Val Tyr Met Arg Asn Phe Lys Tyr Pro Gly Asp Leu
                                          115
                     110
    Val Leu Met Glu Glu Lys Lys Leu Asn Tyr Cys Thr Thr Gly Gln
                                          130
                     125
    Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr
10
                                          145
                     140
    Val Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile
                                          155
                     150
    Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu Tyr Lys Leu
                     165
15
```

 A polypeptide comprising an amino acid sequence represented by the following formula 8 (SEQ ID NO: 8):

formula 8

```
Met Gln Gln Pro Val Asn Tyr Pro Cys Pro Gln Ile Tyr Trp Val
                                           10
25
     Asp Ser Ser Ala Thr Ser Pro Trp Ala Pro Pro Gly Ser Val Phe
                                           25
                       20
     Ser Cys Pro Ser Ser Gly Pro Arg Gly Pro Gly Gln Arg Arg Pro
                       35
                                           40
     Pro Pro Pro Pro Pro Pro Ser Pro Leu Pro Pro Pro Ser Gln
30
                       50
                                           55
     Pro Pro Leu Pro Pro Leu Ser Pro Leu Lys Lys Lys Asp Asn
                                           70
                       65
     Ile Glu Leu Trp Leu Pro Val Ile Phe Phe Met Val Leu Val Ala
                       80
                                           85
35
     Leu Val Gly Met Gly Leu Gly Met Tyr Gln Leu Phe His Leu Gln
                       95
                                          100
     Lys Glu Leu Ala Glu Leu Arg Glu Phe Thr Asn His Ser Leu Arg
                                          115
                      110
     Val Ser Ser Phe Glu Lys Gln Ile Ala Asn Pro Ser Thr Pro Ser
                      125
                                          130
     Glu Thr Lys Lys Pro Arg Ser Val Ala His Leu Thr Gly Asn Pro
                      140
                                          145
     Arg Ser Arg Ser Ile Pro Leu Glu Trp Glu Asp Thr Tyr Gly Thr
                                          160
                      155
45
     Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile
                                          175
                      170
     Asn Glu Ala Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg
                                          190
                      185
     Gly Gln Ser Cys Asn Ser Gln Pro Leu Ser His Lys Val Tyr Met
50
                                          205
                      200
     Arg Asn Phe Lys Tyr Pro Gly Asp Leu Val Leu Met Glu Glu Lys
                                          220
                      215
     Lys Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser Ser
                                          235
                                                               240
                      230
55
```

Tyr Leu Gly Ala Val Phe Asn Leu Thr Val Ala Asp His Leu Tyr
245

Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys
260

Thr Phe Phe Gly Leu Tyr Lys Leu
275

278

70 9. A polypeptide comprising an amino acid sequence represented by the following formula 9 (SEQ ID NO: 9):

formula 9

Ser Val Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr 20 35 Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn 50 55 Gln Pro Leu Asn His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro 70 25 Glu Asp Leu Val Leu Met Glu Glu Lys Arg Leu Asn Tyr Cys Thr 80 Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val Phe 95 100 Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu 30 110 115 Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu Tyr 130 135 Lys Leu 137 35

 A polypeptide comprising an amino acid sequence represented by the following formula 10 (SEQ ID NO: 10):

formula 10

55

```
Pro Glu Asp Leu Val Leu Met Glu Glu Lys Arg Leu Asn Tyr Cys
                       80
     Thr Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val
                                          100
                      95
     Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Ile Ser Gln
                     110
                                          115
                                                               120
     Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu
                      125
                                          130
                                                               135
     Tyr Lys Leu
10
             138
```

11. A polypeptide comprising an amino acid sequence represented by the following formula 11 (SEQ ID NO: 11):

formula 11

- Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe Glu Lys Gln Ile Ala Asn Pro Ser Thr Pro Ser Glu Lys Lys Glu Pro Arg Ser Val Ala His Leu Thr Gly Asn Pro His Ser Arg Ser Ile Pro Leu Glu Trp Glu Asp Thr Tyr Gly Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His Lys Val Tyr Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met Glu Glu Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu Tyr Lys Leu
 - 12. A polypeptide comprising an amino acid sequence represented by the following formula 12 (SEQ ID NO: 12):

formula 12

Met Gln Gln Pro Met Asn Tyr Pro Cys Pro Gln Ile Phe Trp Val

```
10
                                                                 15
     Asp Ser Ser Ala Thr Ser Ser Trp Ala Pro Pro Gly Ser Val Phe
                                                                 30
                                            25
                       20
     Pro Cys Pro Ser Cys Gly Pro Arg Gly Pro Asp Gln Arg Arg Pro
                                                                 45
                       35
     Pro Pro Pro Pro Pro Val Ser Pro Leu Pro Pro Pro Ser Gln
                                                                 60
                                            55
                       50
     Pro Leu Pro Leu Pro Pro Leu Thr Pro Leu Lys Lys Lys Asp His
                                                                 75
                       65
10
     Asn Thr Asn Leu Trp Leu Pro Val Val Phe Phe Met Val Leu Val
                                                                 90
                                            85
                       80
     Ala Leu Val Gly Met Gly Leu Gly Met Tyr Gln Leu Phe His Leu
                                           100
     Gln Lys Glu Leu Ala Glu Leu Arg Glu Phe
                                              Thr Asn Gln Ser Leu
                                           115
                                                                120
                      110
     Lys Val Ser Ser Phe Glu Lys Gln Ile Ala Asn Pro Ser Thr Pro
                                           130
                                                                135
                      125
     Ser Glu Lys Lys Glu Pro Arg Ser Val Ala His Leu Thr Gly Asn
                                           145
                      140
20
     Pro His Ser Arg Ser Ile Pro Leu Glu Trp Glu Asp Thr Tyr Gly
                                           160
                      155
     Thr Ala Leu Ile Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val
                                           175
                                                                180
                      170
     Ile Asn Glu Thr Gly Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe
25
                                           190
                                                                195
                      185
     Arg Gly Gln Ser Cys Asn Asn Gln Pro Leu Asn His Lys Val Tyr
                      200
                                           205
     Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu Val Leu Met Glu Glu
                                           220
                      215
30
     Lys Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser
                                           235
                      230
     Ser Tyr Leu Gly Ala Val Phe Asn Leu Thr Ser Ala Asp His Leu
                                           250
                      245
     Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser
35
                                           265
                                                                270
                      260
                          Leu Tyr Lys Leu
     Lys Thr Phe Phe Gly
                      275
```

13. A polypeptide comprising an amino acid sequence encoded by a nucleotide sequence being capable of hybridyzing with a comprimentary strand of the nucleotide sequence encoding at least one amino acid sequence selected from the group of the amino acids sequences represented by said formula 1, 5 and 9 (SEQ ID NOS: 1, 5 and 9).

- 14. A polypeptide comprising an amino acid sequence encoded by a nucleotide sequence being capable of hybridyzing with a comprimentary strand of at least one nucleotide sequence selected from the group of the nucleotide sequences represented by SEQ ID NOS: 13, 17 and 21.
- 50 15. The polypeptide according to any one of claims 1 to 14, wherein the polypeptide is capable of binding to Fas antigen.
 - 16. The polypeptide according to any one of claims 1 to 15, wherein the polypeptide has activity inducing apoptosis of a Fas antigen-expressing cell.
 - 17. The polypeptide according to any one of claims 1 to 16, wherein the polypeptide is obtained by genetic engineering techniques.

- 18. A polypeptide comprising a part of an amino acid sequence represented by the aforementioned formula 4 (SEQ ID NO: 4).
- A polypeptide comprising a part of an amino acid sequence represented by the aforementioned formula 8 (SEQ ID NO: 12).
 - 20. A polypeptide comprising a part of an amino acid sequence represented by the aforementioned formula 12 (SEQ ID NO: 12).
- 21. A fusion polypeptide being fused with each other at least two polypeptides comprising a part of an amino acid sequence represented by the aforementioned formulae 4, 8 or 12 (SEQ ID NOS: 4, 8 or 12).
 - 22. The polypeptide according to any one of claims 18 to 21, wherein the polypeptide binds to Fas antigen.
- 15 23. A DNA comprising a nucleotide sequence encoding the polypeptide according to any one of claims 1 to 22
 - 24. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 13 (SEQ ID NO: 13):

formula 13

20

AAA GTG GCC CAT TTA ACA GGC AAG TCC AAC TCA AGG TCC ATG CCT 45 CTG GAA TGG GAA GAC ACC TAT GGA ATT GTC CTG CTT TCT GGA GTG 90 AAG TAT AAG AAG GGT GGC CTT GTG ATC AAT GAA ACT GGG CTG TAC 135 TTT GTA TAT TCC AAA GTA TAC TTC CGG GGT CAA TCT TGC AAC AAC 180 30 CTG CCC CTG AGC CAC AAG GTC TAC ATG AGG AAC TCT AAG TAT CCC 225 CAG GAT CTG GTG ATG ATG GAG GGG AAG ATG ATG AGC TAC TGC ACT 270 ACT GGG CAG ATG TGG GCC CGC AGC AGC TAC CTG GGG GCA GTG TTC 315 AAT CTT ACC AGT GCT GAT CAT TTA TAT GTC AAC GTA TCT GAG CTC 360 405 TCT CTG GTC AAT TTT GAG GAA TCT CAG ACG TTT TTC GGC TTA TAT 411 AAG CTC

25. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 14 (SEQ ID NO: 14):

formula 14

AGG AAA GTG GCC CAT TTA ACA GGC AAG TCC AAC TCA AGG TCC ATG 45

	CCT	CTG	GAA	TGG	GAA	GAC	ACC	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	90
	GTG	AAG	TAT	AAG	AAG	GGT	GGC	CTT	GTG	ATC	AAT	GAA	ACT	GGG	CTG	135
5	TAC	TTT	GTA	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAA	TCT	TGC	AAC	180
	AAC	CTG	ccc	CTG	AGC	CAC	AAG	GTC	TAC	ATG	AGG	AAC	TCT	AAG	TAT	225
	CCC	CAG	GAT	CTG	GTG	ATG	ATG	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	270
10	ACT	ACT	GGG	CAG	ATG	TGG	GCC	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	315
	TTC	AAT	CTT	ACC	AGT	GCT	GAT	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	360
5	CTC	TCT	CTG	GTC	AAT	TTT	GAG	GAA	TCT	CAG	ACG	TTT	TTC	GGC	TTA	405
	TAT	AAG	CTC													414

26. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 15 (SEQ ID NO: 15):

formula 15

25 CAG CTC TTC CAC CTA CAG AAG GAG CTG GCA GAA CTC CGA GAG TCT 45 ACC AGC CAG ATG CAC ACA GCA TCA TCT TTG GAG AAG CAA ATA GGC 90 CAC CCC AGT CCA CCC CCT GAA AAA AAG GAG CTG AGG AAA GTG GCC 135 CAT TTA ACA GGC AAG TCC AAC TCA AGG TCC ATG CCT CTG GAA TGG 180 GAA GAC ACC TAT GGA ATT GTC CTG CTT TCT GGA GTG AAG TAT AAG 35 AAG GGT GGC CTT GTG ATC AAT GAA ACT GGG CTG TAC TTT GTA TAT 270 TCC AAA GTA TAC TTC CGG GGT CAA TCT TGC AAC AAC CTG CCC CTG 315 AGC CAC AAG GTC TAC ATG AGG AAC TCT AAG TAT CCC CAG GAT CTG 360 40 GTG ATG ATG GAG GGG AAG ATG ATG AGC TAC TGC ACT ACT GGG CAG 405 ATG TGG GCC CGC AGC AGC TAC CTG GGG GCA GTG TTC AAT CTT ACC 450 AGT GCT GAT CAT TTA TAT GTC AAC GTA TCT GAG CTC TCT CTG GTC 495 AAT TTT GAG GAA TCT CAG ACG TTT TTC GGC TTA TAT AAG CTC 537

50 27. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 16 (SEQ ID NO: 16):

	-	7	_	7	_
$_{\perp}$	rm	$u \perp$	۵.	1	O

	ATG	CAG	CAG	CCC	TTC	AAT	TAC	CCA	TAT	CCC	CAG	ATC	TAC	TGG	GTG	45
5	GAC	AGC	AGT	GCC	AGC	TCT	ccc	TGG	GCC	CCT	CCA	GGC	ACA	GTT	CTT	90
•	ccc	TGT	CCA	ACC	TCT	GTĢ	ccc	AGA	AGG	CCT	GGT	CAA	AGG	AGG	CCA	135
10	CCA	CCA	CCA	CCG	CCA	CCG	CCA	CCA	CTA	CCA	ССТ	CCG	CCG	CCG	CCG	180
	CCA	CCA	CTG	CCŢ	CCA	CTA	CCG	CTG	CCA	ccc	CTG	AAG	AAG	AGA	GGG	225
	AAC	CAC	AGC	ACA	GGC	CTG	TGT	CTC	CTT	GTG	ATG	TTT	TTC	ATG	GTT	270
15	CTG	GTT	GCC	TTG	GTA	GGA	TTG	GGC	CTG	GGG	ATG	TTT	CAG	CTC	TTC	315
	CAC	CTA	CAG	AAG	GAG	CTG	GCA	GAA	CTC	CGA	GAG	TCT	ACC	AGC	CAG	360
20	ATG	CAC	ACA	GCA	TCA	TCT	TTG	GAG	AAG	CAA	ATA	GGC	CAC	ccc	AGT	405
20	CCA	ccc	CCT	GAA	AAA	AAG	GAG	CTG	AGG	AAA	GTG	GCC	CAT	TTA	ACA	450
	GGC	AAG	TCC	AAC	TCA	AGG	TCC	ATG	CCT	CTG	GAA	TGG	GAA	GAC	ACC	495
25	TAT	GGA	ATT	GTC	CTG	CTT	TCT	GGA	GTG	AAG	TAT	AAG	AAG	GGT	GGC	540
	CTT	GTG	ATC	AAT	GAA	ACT	GGG	CTG	TAC	TTT	GTA	TAT	TCC	AAA	GTA	585
	TAC	TTC	CGG	GGT	CAA	TCT	TGC	AAC	AAC	CTG	ccc	CTG.	AGC	CAC	AAG	630
30	GTC	TAC	ATG	AGG	AAC	TCT	AAG	TAT	CCC	CAG	GAT	CTG	GTG	ATG	ATG	675
	GAG	GGG	AAG	ATG	ATG	AGC	TAC	TGC	ACT	ACT	GGG	CAG	ATG	TGG	GCC	720
35	CGC	AGC	AGC	TAC	CTG	GGG	GCA	GTG	TTC	AAT	CTT	ACC	AGT	GCT	GAT	765
	CAT	TTA	TAT	GTC	AAC	GTA	TCT	GAG	CTC	TCT	CŢĢ	GTC	AAT	TTT	GAG	810
	GAA	TCT	CAG	ACG	TTT	TTC	GGC	TTA	TAT	AAG	CTC				-	843

40

28. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 17 (SEQ ID NO: 17):

45 formula 17

AGT GTG GCC CAC TTA ACA GGG AAC CCC CGC TCA AGG TCC ATC CCT 45

50

	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	ACT	GCT	TTG	ATC	TCT	GGA	GTG	90
·	AAG	TAT	AAG	AAA	GGC	GGC	CTT	GTG	ATC	AAT	GAG	GCT	GGG	TTG	TAC	135
5	TTC	GTA	TAT	TCC	AAA,	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AGC	180
	CAG	ccc	CTA	AGC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TTT	AAG	TAT	CCT	225
10	GGG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	AAG	TTG	AAT	TAC	TGC	ACT	270
U	ACT	GGC	CAG	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTA	GGG	GCA	GTA	TTT	315
	AAT	CTT	ACC	GTT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	CTC	360
15	TCT	CTG	ATC	AAT	ŢŢŢ	GAG	GAA	TCT	AAG	ACC	TTT	TTT	GGC	TTA	TAT.	405
	AAG	CTT														411

29. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 18 (SEQ ID NO: 18):

formula 18

	AGG	AGT	GTG	GCC	CAC	TTA	ACA	GGG	AAC	ccc	CGC	TCA	AGG	TCC	ATC	45
	CCT	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	ACT	GCT	TTG	ATC	TCT	GGA	90
10	GTG	AAG	TAT	AAG	AAA	GGC	GGC	CTT	GTG	ATC	AAT	GAG	GCT	GGG	TTG	135
	TAC	TTC	GTA	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	180
	AGC	CAG	ccc	CTA	AGC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TTT	AAG	TAT	225
15	CCT	GGG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	AAG	TTG	AAT	TAC	TGC	270
	ACT	ACT	GGC	CAG	ATA	TGG	GCC	CAC	AGC	AGÇ	TAC	CTA	GGG	GCA	GTA	315
ю	TTT	AAT	CTT	ACC	GTT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	360
	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTT	GGC	TTA	405
	TAT	AAG	CTT													414

45

30. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 19 (SEQ ID NO: 19):

50

formula 19

	CAA	CTC	TTT	CAT	CTA	CAG	AAG	GAA	CTG	GCA	GAA	CTC	CGT	GAG	TTC	45
5	ACC	AAC	CAC	AGC	CTT	AGA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	ATA	GCC	90
	AAC	ccc	AGC	ACA	ccc	TCT	GAA	ACC	AAA	AAG	CCA	AGG	AGT	GTG	GCC	135
	CAC	TTA	ACA	GGG	AAC	ccc	CGC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	180
10	GAA	GAC	ACA	TAT	GGA	ACT	GCT	TTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	225
	AAA	GGC	GGC	CTT	GTG	ATC	AAT	GAG	GCT	GGG	TTG	TAC	TTC	GTA	TAT	270
15	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AGC	CAG	ccc	CTA	315
	AGC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TTT	AAG	TAT	CCT	GGG	GAT	CTG	360
	GTG	CTA	ATG	GAG	GAG	AAG	AAG	TTG	AAT	TAC	TGC	ACT	ACT	GGC	CAG	405
20	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTA	GGG	GCÁ	GTA	TTT	AAT	CTT	ACC	450
	GTT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	495
25	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTT	GGC	TTA	TAT	AAG	CTT		537

31. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 20 (SEQ ID NO: 20):

formula 20

ATG CAG CAG CCC GTG AAT TAC CCA TGT CCC CAG ATC TAC TGG GTA 45 35 GAC AGC AGT GCC ACT TCT CCT TGG GCT CCT CCA GGG TCA GTT TTT 90 TCT TGT CCA TCC TCT GGG CCT AGA GGG CCA GGA CAA AGG AGA CCA 135 CCG CCT CCA CCA CCT CCA TCA CCA CTA CCA CCG CCT TCC CAA 180 CCA CCC CCG CTG CCT CCA CTA AGC CCT CTA AAG AAG AAG GAC AAC 225 ATA GAG CTG TGG CTA CCG GTG ATA TTT TTC ATG GTG CTG GTG GCT 270 CTG GTT GGA ATG GGG TTA GGA ATG TAT CAA CTC TTT CAT CTA CAG 45 AAG GAA CTG GCA GAA CTC CGT GAG TTC ACC AAC CAC AGC CTT AGA 360 GTA TCA TCT TTT GAA AAG CAA ATA GCC AAC CCC AGC ACA CCC TCT 405 50 GAA ACC AAA AAG CCA AGG AGT GTG GCC CAC TTA ACA GGG AAC CCC

55

	CGC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	ACT	495
	GCT	TTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	AAA	GGC	GGC	CTT	GTG	ATC	540
5	AAT	GAG	GCT	GGG	TTG	TAC	TTC	GTA	TAT	TCC	AAA	GTA	TAC	TTC	CGG	585
	GGT	CAG	TCT	TGC	AAC	AGC	CAG	ccc	CTA	AGC	CAC	AAG	GTC	TAT	ATG	630
	AGG	AAC	TTT	AAG	TAT	CCT	GGG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	675
0	AAG	TTG	AAT	TAC	TGC	ACT	ACT	GGC	CAG	ATA	TGG	GCC	CAC	AGC	AGC	720
	TAC	CTA	GGG	GCA	GTA	TTT	AAT	CTT	ACC	GTT	GCT	GAC	CAT	TTA	TAT	765
5	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	810
	ACC	TTT	TTT	GGC	TTA	TAT	AAG	CTT								834

32. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 21 (SEQ ID NO: 21):

formula 21

25	AGT	GTG	GCC	CAT	TTA	ACA	GGG	AAC	CCC	CAC	TCA	AGG	TCC	ATC	CCT	4.5
	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	ACC	GCT	CTG	ATC	TCT	GGA	GTG	90
30	AAG	TAT	AAG	AAA	GGT	GGC	CTT	GTG	ATC	AAC	GAA	ACT	GGG	TTG	TAC	135
••	TTC	GTG	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AAC	180
	CAG	ccc	CTA	AAC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TCT	AAG	TAT	CCT	225
35	GAG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	AGG	TTG	AAC	TAC	TGC	ACT	270
	ACT	GGA	CAG	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTG	GGG	GCA	GTA	TTC	315
40	AAT	CTT	ACC	AGT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	CTC	360
	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTC	GGC	TTG	TAT	405
	AAG	CTT														411

33. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 22 (SEQ ID NO: 22):

50

formula 22

								-								
5	AGG	AGT	GTG	GCC	CAT	TTA	ACA	GGG	AAC	CCC	CAC	TCA	AGG	TCC	ATC	45
	CCT	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	ACC	GCT	CTG	ATC	TCT	GGA	90
	GTG	AAG	TAT	AAG	AAA	GGT	GGC	CTT	GTG	ATC	AAC	GAA	ACT	GGG	TTG	135
0	TAC	TTC	GTG	TAT	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	180
	AAC	CAG	ccc	CTA	AAC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TCT	AAG	TAT	225
5	CCT	GAG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	AAG	AGG	TTG	AAC	TAC	TGC	270
	ACT	ACT	GGA	CAG	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTG	GGG	GCA	GTA	315
ro	TTC	AAT	CTT	ACC	AGT	GCT	GAC	CAT	TTA	TAT	GTC	AAC	ATA	TCT	CAA	360
	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTC	GGC	TTG	405
	TAT	AAG	CTT													414

25 34. The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 23 (SEQ ID NO: 23):

formula 23

30	CAG	CTC	TTC	CAC	CTG	CAG	AAG	GAA	CTG	GCA	GAA	CTC	CGT	GAG	TTC	45
	ACC	AAC	CAA	AGC	CTT	AAA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	ATA	GCC	90
35	AAC	CCC	AGT	ACA	ccc	TCT	GAA	AAA	AAA	GAG	CCG	AGG	AGT	GTG	GCC	135
	CAT	TTA	ACA	GGG	AAC	ccc	CAC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	180
	GAA	GAC	ACA	TAT	GGA	ACC	GCT	CTG	ATC	TCT	GGA	GTG	AAG	TAT	AAG	225
40	AAA	GGT	GGC	CTT	GTG	ATC	AAC	GAA	ACT	GGG	TTG	TAC	TTC	GTG	TAT	270
	TCC	AAA	GTA	TAC	TTC	CGG	GGT	CAG	TCT	TGC	AAC	AAC	CAG	ccc	CTA	315
	AAC	CAC	AAG	GTC	TAT	ATG	AGG	AAC	TCT	AAG	TAT	ССТ	GAG	GAT	CTG	360
45	GTG	CTA	ATG	GAG	GAG	AAG	AGG	TTG	AAC	TAC	TGC	ACT	ACT	GGA	CAG	405
	ATA	TGG	GCC	CAC	AGC	AGC	TAC	CTG	GGG	GCA	GTA	TTC	AAT	CTT	ACC	450
50	AGT	GCT	GAC	CAT	TTA	TAT	GTC.	AAC	ATA	TCT	CAA	CTC	тст	CTG	ATC	495
	AAT	TTT	GAG	GAA	TCT	AAG	ACC	TTT	TTC	GGC	TTG	TAT	AAG	CTT		537

^{35.} The DNA according to claim 23 comprising the nucleotide sequence represented by the following formula 24 (SEQ ID NO: 24):

formula 24

	ATG	CAG	CAG	ccc	ATG	AAT	TAC	CCA	TGT	ccc	CAG	ATC	TTC	TGG	GTA	45
5	GAC	AGC	AGT	GCC	ACT	TCA	TCT	TGG	GCT	CCT	CCA	GGG	TCA	GTT	TTT	90
	ccc	TGT	CCA	TCT	TGT	GGG	CCT	AGA	GGG	CCG	GAC	CAA	AGG	AGA	CCG	135
	CCA	CCT	CCA	CCA	CCA	CCT	GTG	TCA	CCA	CTA	CCA	CCG	CCA	TCA	ÇAA	180
10	CCA	CTC	CCA	CTG	CCG	CCA	CTG	ACC	CCT	CTA	AAG	AAG	AAG	GAC	CAC	225
	AAC	ACA	AAT	CTG	TGG	CTA	CCG	GTG	GTA	TTT	TTC	ATG	GTT	CTG	GTG	270
15	GCT	CTG	GTT	GGA	ATG	GGA	TTA	GGA	ATG	TAT	CAG	CTC	TTC	CAC	CTG	315
	CAG	AAG	GAA	CTG	GCA	GAA	CTC	CGT	GAG	TTC	ACC	AAC	CAA	AGC	CTT	360
	AAA	GTA	TCA	TCT	TTT	GAA	AAG	CAA	ATA	GCC	AAC	CCC	AGT	ACA	CCC	405
20	TCT	GAA	AAA	AAA	GAG	CCG	AGG	AGT	GTG	GCC	CAT	TTA	ACA	GGG	AAC	450
	CCC	CAC	TCA	AGG	TCC	ATC	CCT	CTG	GAA	TGG	GAA	GAC	ACA	TAT	GGA	495
	ACC	GCT	CTG	ATC	TÇT	GGA	GTG	AAG	TAT	AAG	AAA	GGT	GGC	CTT	GTG	540
25	ATC	AAC	GAA	ACT	GGG	TTG	TAC	TTC	GTG	TAT	TCC	AAA	GTA	TAC	TTC	585
	CGG	GGT	CAG	TCT	TGC	AAC	AAC	CAG	CCC	CTA	AAC	CAC	AAG	GTC	TAT	630
30	ATG	AGG	AAC	TCT	AAG	TAT	CCT	GAG	GAT	CTG	GTG	CTA	ATG	GAG	GAG	675
	AAG	AGG	TTG	AAC	TAC	TGC	ACT	ACT	GGA	CAG	ATA	TGG	GCC	CAC	AGC	720
	AGC	TAC	CTG	GGG	GCA	GTA	TTC	AAT	CTT	ACC	AGT	GCT	GAC	CAT	TTA	765
35	TAT	GTC	AAC	ATA	TCT	CAA	CTC	TCT	CTG	ATC	AAT	TTT	GAG	GAA	TCT	810
	AAG	ACC	TTT	TTC	GGC	TTG	TAT	AAG	CTT							837

- 36. The DNA according to claim 23 comprising a part of the nucleotide sequence represented by the aforementioned formula 16 (SEQ ID NO: 16).
- 37. The DNA according to claim 23 comprising a part of the nucleotide sequence represented by the aforementioned formula 20 (SEQ ID NO: 20).
 - 38. The DNA according to claim 23 comprising a part of the nucleotide sequence represented by the aforementioned formula 24 (SEQ ID NO: 24).
- 39. A DNA being capable of hybridyzing with a comprimentary strand of at least one nucleotide sequence selected from the group of the nucleotide sequences represented by the aforementioned formulae 13, 17 or 21 (SEQ ID NOS: 13, 17 or 21), and encoding a Fas ligand.
 - 40. A recombinant DNA molecule comprising the DNA fragment of any one of claims 23 to 39.
 - 41. A transformant which is transformed with the DNA of any one of claims 23 to 39.
 - 42. A transformant which is transformed with the recombinant DNA molecule of claim 40.

- 43. The transformant according to claim 41 or 42, wherein a host of said transformant is selected from the group consisting of a) E.coli, b) yeast and c) mammalian cells.
- 44. A process for producing the polypeptide of any one of claims 1 to 22 which comprises culturing the transformant of any one of claims 41 to 43, and recovering and purifying said polypeptide from the culture mixture.
- 45. A process for purifying the polypeptide of any one of claims 1 to 22 from a sample containing said polypeptide, wherein said process involves at least one purification selected from (1) an affinity chromatography in which Fas antigen is used, and (2) an affinity chromatography in which an antibody which recognizes the polypeptide of any one of claims 1 to 22 is used.
 - 46. An antibody which recognizes the polypeptide of any one of claims 1 to 22.

5

10

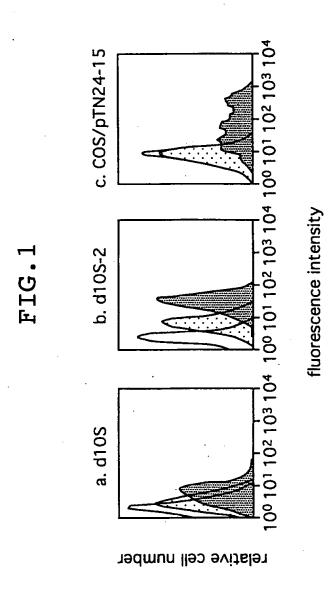
30

45

50

- 15 47. The antibody according to claim 46 wherein said antibody is a monoclonal antibody.
 - 48. The antibody according to claim 46 wherein said antibody is a polyclonal antibody.
- 49. The antibody according to any one of claims 46 to 48 wherein said antibody has an effect of inhibiting apoptosis of Fas antigen-expressing cell.
 - 50. An oligonucleotide or a derivative thereof which comprises a nucleotide sequence complementary to a part of the gene of a Fas ligand or a part of mRNA for a Fas ligand.
- 51. The oligonucleotide or a derivative thereof according to claim 50 wherein said oligonucleotide or its derivative regulates expression of a Fas ligand.
 - 52. The oligonucleotide or a derivative thereof according to claim 50 or 51 wherein said oligonucleotide or its derivative inhibits expression of the Fas ligand.
 - 53. The oligonucleotide or a derivative thereof according to any one of claims 50 to 52 wherein said oligonucleotide or its derivative comprises a part of a nucleotide sequence which is complementary to any one of nucleotide sequences of SEQ ID NOS: 13 to 28 and ID SEQ NOS: 31 to 32.
- 54. A method for screening a substance related to a Fas ligand or a Fas antigen which comprises using at least a polypeptide according to any one of claims 1 to 22 or a transformant expressing thereof.
 - 55. The method for screening a substance related to a Fas ligand or a Fas antigen according to claim 54 which further comprises using Fas antigen, or a Fas antigen-expressing cell.
 - 56. The screening method according to claim 54 or 55 wherein a substance to be screened is selected from the group consisting of a substance which bind to said Fas ligand, which exert influence upon expression of said Fas ligand, which exert influence upon expression of said Fas antigen and which exert influence upon action of said Fas ligand on its target cells.
 - 57. The screening method according to any one of claims 54 to 56 wherein said method includes a step selected from the following steps (1) to (3)
 - (a) at least one selected from the group consisting of polypeptides according to claims 1 to 22 transformants expressing thereof and culture supernatant of the transformants is cultured together with cells which express Fas antigen,
 - (b) a substance to be tested or a sample containing the substance to be tested is added to the above system (a), and
 - (c) at least 1 item selected from viability, morphological changes and biochemical changes in the Fas antigen-expressing cells is measured,
 - (a) a substance to be tested or a sample containing the substance to be tested is incubated together with at least one selected from the group consisting of polypeptides according to claims

	1 to 22, transformants expressing thereof and culture supernatant of the transformants, (b) cells which express Fas antigen are added to the above system (a), and cultured, and (c) at least 1 item selected from viability, morphological changes and biochemical changes in the Fas antigen-expressing cells is measured, and
5	 (a) a substance to be tested or a sample containing the substance to be tested is incubated together with cells which express Fas antigen, (b) at least one selected from the group consisting of polypeptides according to claims 1 to 22,
10	transformants expressing thereof and culture supernatants of the transformants is added to the above system (a) and cultured, and
	(c) at least 1 item selected from viability, morphological changes and biochemical changes in the Fas antigen-expressing cells is measured.
15	
20	
25	
30	
35	
33	
40	
4 5	
50	
55	



FTG.2

CCT Pro Pro So ICAGAGTCCTGTCCTTGACACTTCAGTCTCCACAAGACTGAGAAGGAAACCCTTTCCTGGGGCTGGGTGCC AAC Asn CAN Glass 1881 250 Pro 150 LÝ8 Asn 200 NAG Lyb GPA Glu GTT Val SCT Ala CCA Pro GAC Asp ቸች ቸ TT. Phe AAC Asn NAG Lys 73C 27.8 GAG Glu TTT.AAT CTT ACC AAG Lys 75G CCA ATG Met 666 617 TAT TYF GAG TCT Ser TCT Ser AAG. Lys CCT CCT AAG Lys 9 9 9 9 TCA ACA CAG ATG Met S S S S TCT Ser AAG Lys TTA GGT Gly CTA GTA GIG TTA GCC ACT Ala Thr 20 800 TAC CTA GGG GCA GTA Tyr Leu Gly Ala Val CCA Pro CTA Leu 20 AGA Arg CAC His CGG Arg GTG Val 666 61y 6314 6314 AGA Arg CCT Pro CT. SCC Ala Trc Phe TCT ATG Wet CCT GGG GAT CTG Pro Gly Asp Leu 650 AAA GTA TAC 1 Lys Val Tyr F 350 GTT GGA Val Gly P 200 CAA AGG J Gln Arg J CTA AGC Leu Ser AGT GTG Ser Val CAC AGC His Ser AGT GCT TTG ATC AGC GAC GGA Gly Asn Asn CCA Pro CTG Leu AGG TCC Ser 190 TAT £ 2 CG CCA Pro Acc Act AGC Ser 240 GTA CCT Pro Ala TGG 966 614 CTC Leu TTC Phe AAG Lys 634 614 TAT Tyr AAG Lys AGC GTG Val TAC AGA Arg cyc cyc AAA Lys ACA TAT Thr Tyr TTC GTA Phe Val CCC TTT Phe re Lea ACT ACT GGC CAG ATA TGG GCC CAC Thr Thr Gly Gln Ile Trp Ala His ATC r F Asn Asn CCC Pro GTG CGT Acc TTC TAC ATG AGG Met Arg 210 CTC GAC CAG Gln 666 61y Prop C gy Str ATG Met S G G TCT Ser CAA Gla TTC Phe GAA Glu 110 TCT Ser GAA G1u 160 160 公3 TCC Ser CCC Pro TAT TYF 250 TCC Ser TTT 4 CC 6 550 TGG Trp 666 G1y CC Pro CCA Pro gyr Glu Ala Ala CCT ATA Ile င် င်ဒီ ACA AAG GTC Lys Val GAG TAC Tyr 161 Cys CCG GTC SPA Cla AGC Crc Leu AAT AAT Asn CAC TCT Ser CCA Pro CCG Pro CCC Pro CCT Pro AAG Lys GTG Val TTT Phe Le CT CAG Gln AAC Asn ATC Ile CTA ATC AGC CCC Pro GTT CCA TGG Trp CTA GCC Ala TCC GTG Val CTA TTG AAT TAC Leu Asn Tyr cyc cyc CTT CCC TCA Ser CTG Leu CAT TCA Ser ATA Ile AGG Cyc cyc 00 01 01 01 666 61y CC. GAG Glu TTT Phe Sta Sta TCA Ser 9 61 7 150 AAG Lys 600 GGC Gly CCA Pro CCT 300 ATA Ile 750 AAG Lys

FTG,3

850 GCT GAC CAT TTA TAT GTC AAC ATA TCT CTC TCT CTG ATC AAT TTT GAG GAA TCT AAG ACC TTT TTT GGC TTA Ala Asp His Leu Tyr Val Asn Ile Ser Gln Leu Ser Leu Ile Asn Phe Glu Glu Ser Lys Thr Phe Phe Gly Leu 260 950 TAT AAG CTT TAA AGGAAAAAGCATTTTAGAATGATCTATTATTCTTTATCATGGATGCCAGGAATATTGTCTTCAATGAGAGTCTTCAAGACC Tyr Lys Leu *** 1000 AATTGAGCCACAAAGACCACAAGGTCCAACAGGTCAGCTACCCTTCATTTTCTAGAGGTCCATGGAGTGGTCCTTAATGCCTGCATCATGAGCCAGATG TATGACTATACAAGGGTGAGAAAGGATGCTAGGTTTCATGGATAAGCTAGAGACTGAAAAAAGCCAGTGTCCCATTGGCATCATCTTTATTTTAACTG **ATGITITICIGAGCCCACCITIGAIGCIAACAGAGAAAIAAGAGGGIGITITIGAGGCACAAGICAITICICIACAIAGCAIGIGIACCICCAGIGCAAIGA** TGTCTGTGTGTTTTTATGTATGAGAGTAGAGCGATTCTAAAGAGTCACATGAGTACAACGCGTACATTACGGAGTACATATTAGAAACGTATGTGTT ACATITGAIGCTAGAAIAICIGAAIGITICIIGCIA

FIG.4

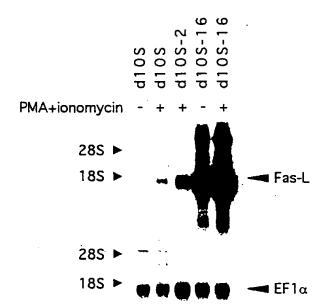


FIG.5

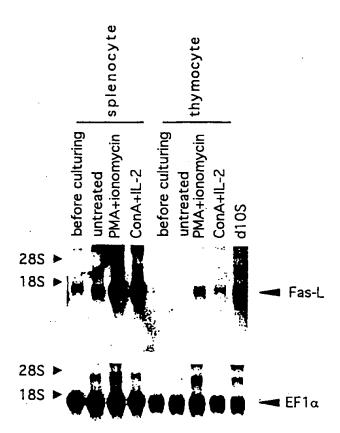


FIG.6

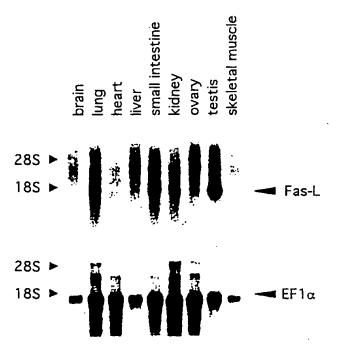


FIG.7

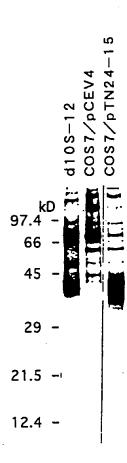
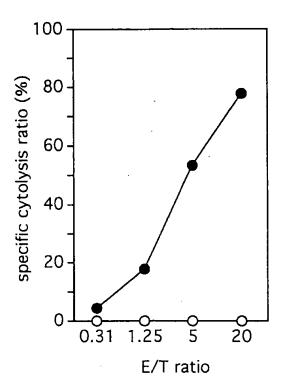


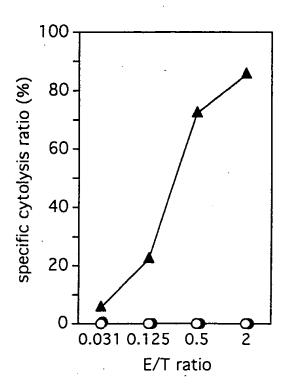
FIG.8



effector cell: d10S target cell: W4

-o- effector cell : d10S target cell : WR19L

FIG.9

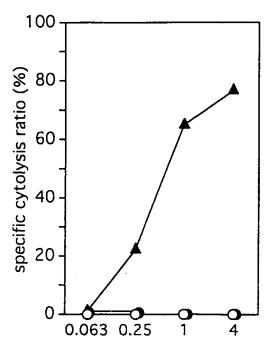


effector cell : COS/pCEV4 target cell : W4

effector cell: COS/pTN24-15 target cell: W4

effector cell: COS/pTN24-15 target cell: WR19L

FIG. 10



concentration of culture supernatant added (fold)

effector cell : COS/pTN24-15 target cell : W4

effector cell : COS/pTN24-15 target cell : WR19L

effector cell : COS/pCEV4 target cell : W4

FIG.11

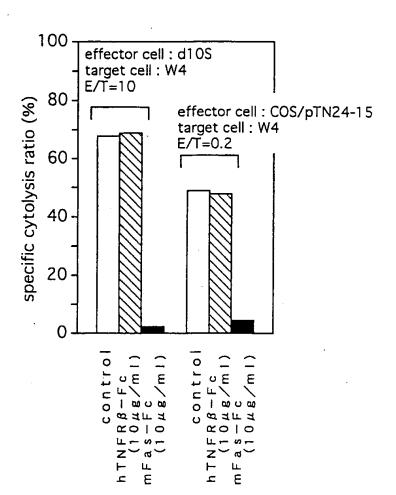
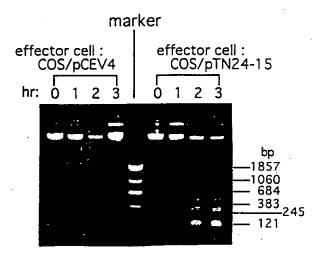


FIG.12



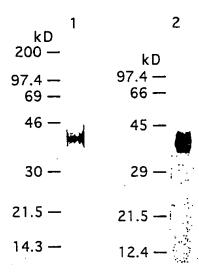
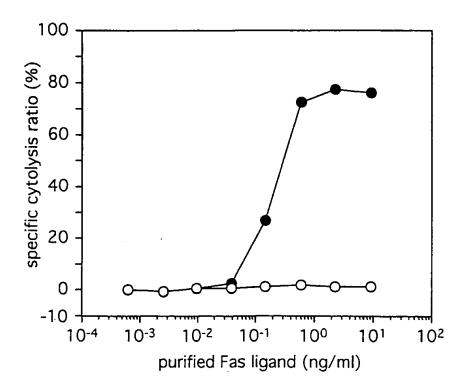


FIG.14



-0- target cell : WR19L

-- target cell : W4

${ m FIG}$. 15

G1y GGG	Leu CTG	Glu GGG A	Ala GCA	val Grc	Leu CTC TAA GAGAAGCACTTTGGGATTC
Ala Thr ACT G	Pro		GGG		NGGG1
GAA GAA	Gln Leu CTG	Met ATG	Leu	Ser TCT	CTT
	Ser Asn AAC	Met ATG		Leu CTC	AGCA
Ile	Asn AAC	Val	Ser	G1n G1u GAG C.A	GAGA
	Cys TGC	Leu CTG	Ser	Ser TCT	TAA
	Ser	Asp Gat	His Arg CGC	Ile Val GTA	
Gly GGC	Gln CAA	61n 61n 66 66	Ala GCC	Asn AAC	Lys
Gly GGT O	Gly GGT	Pro CCC	Trp TGG		Tyr TAT
Lys AAG	Arg CGG	Tyr TAT	Ile Met ATG	$\mathbf{r}_{\mathbf{y}r}$	Leu TTA
Lys AAG	Phe TTC	Lys Aag	Gln	Leu TTA	61y 66C
Туг ТАТ	Tyr Tac	Phe Ser TCT	61 <i>y</i> 666 0	His	Phe TTC
Lys AAG		Asn	Thr ACT	Asp Gat C	Phe TTT
Val GrG	Lys Aaa	Arg	Thr	Ala GCT	Thr Acc
G1y GGA	Ser	Met ATG	Cys TGC	Ser AGT GT	Lys Gln CAG
Ser TCT	Tyr Tat	Tyr TAC		Thr	Ser
Leu CTT	Val GTA	val GTC	Asn Ser AGC	Leu CTT	Glu GAA
Leu CTG	Phe TYYY C	Ly's AAG	Leu Met ATG	Asn AAT	Glu GAG
Ala Val CT	Tyr Tac	His CAC	Lys Met ATG	h TC	Phe TTT
Thr Ile ATT	Leu CTG T	Ser	Lys AAG	val GTG	Asn AAT
	Ala Ile Asn Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr Grc Crc Crr Gra Gra Gra Tar And And Gra Gcr Crc Crr Gra Arc And Gra Gra Gcr Crc Crr Gra Arc And Gra	Ala Leu Leu Ser Gly Val Lys Tyr Lys Gly Gly Leu Val Ile Asn Glu Thr GTC CTG CTT TCT GGA GTG AAG TAT AAG AAG GGT GGC CTT GTG ATC AAT GAA ACT CT T A C A C T A C A C T A C A C	$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	Ala Leu Leu Crr Gra Gra Gra Tar Ara Ara Gra Gra Gra Gra Gra Gra Tar Trr Gra Tar Trr Gra Trr Gra Trr Gra Trr Gra Trr Gra Trr Gra Trr Trr	Alia

EP 0 675 200 A1

TACCCCCATGCTGACCTGCTGCAGGATCCCCAGGAAGGTGAGCATAGCCTACTAACCTGTTTGGGTAGCACAGGGACAACTGAGGCCTTGAAGG AAGCAGAATCAGAGAGAGAGATAGAGAAAAGAGAAAAGACAGAGGTGTTTCCCTTAGCTATGGAAACTCTATAAAGAGAGATCCAGCTTGCCTCCTCTTG AGCAGTCAGCAACAGGGTCCCGTCCTTGACACCTCAGCCT<u>CTACAGGACTGAGAAGAAGAA</u>AAACGGTTTGCTGGGGGTGGCGTGACTCACCAGCTGC

r CC Ala GCC GIN GIN Pro Phe Asn Tyr Pro Tyr Pro GIN Ile Tyr Trp Val Asp Ser Ser Ala Ser Ser Pro Trp CAG CAG CCC Trc AAT TAC CCA TAT CCC CAG ATC TAC TGG GTG GAC AGC AGT GCC AGG TCT CCC TGG

Pro Pro Pro Pro Pro CCA CCA CCA CCG CCA Pro CCA Gln Arg Arg 40 Pro Arg Arg Pro Gly CCC AGA AGG CCT GGT Cys Pro Thr Ser Val TGT CCA ACC TCT GTG Thr Val Leu Pro ACA GTT CTT CCC င် ဗ Pro

9

100 915 936 GCC Phe Phe Het Val Leu Val Ala Leu Val Gly Leu Gly Leu TTT TTC ATG GTT CTG GTT GCC TTG GTA GGA TTG GGC CTG Pro Pro Leu Lys Lys Arg CCA CCC CTG AAG AAA AGA teu CTC Leu Pro CTA CCG Pro Pro CCT CCA Leu Pro Pro Pro Pro Pro Pro Pro Leu CTA CCA CCT CCG CCG CCG CCA CCA CTG Met ATG 00 Asn His Ser Thr Gly Leu Cys Leu Leu Val AAC CAC AGC ACA GGC CTG TGT CTC CTT GTG CC. Pro CCA

Het Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala Glu Leu Arg Glu ATG TYT CAG CYC TYC CAC CYA CAG AAG GAG CYG GCA GAA CYC CGA GAG GYAAGCCYGCCGGCAGACYGCTGCCTGCCTGGAGGC accaggcataaggggatggaggggccactgggg......gatitciggcittatggttaagaatttattattattataggattttg

Ser Thr Ser Gln Het His Thr Ala Ser Leu Glu Lys Gln Ile G TTTCTGTTTTACTAG TCT ACC AGG ATG CAC ACA GCA TCA TCT TTG GAG AAG CAA ATA G GTGAGTCTTTTTTCGCATGTA

Cattgagttcccaaagatgatctcagcacagaactatgttaatggaatgccttaaattcccacacctttggttcccaactttggtttctgtacacttttaagaggaatt

EP 0 675 200 A1

FIG. 1

······TTCCCACCAAAATAATAGTTGCTATTTTCATTTTTAACATATATTTTTCCTCTC'TCTATGATACAĞ

Ü

His Pro Ser Pro Pro Glu Lys Lys Glu Leu Arg Lys Val Ala His Leu Thr G CAC CCC AGT CCA CCC CCT GAA AAA AAG GAG CTG AGG AAA GTG GCC CAT TTA ACA G GTCTGTATC ည္ကပ္တ

CITGGATTTGGCTTTTCCTTCAGGAAAGGACTTCAAAGCCTAGCAGATTTGGTGCTAGTTCTGAAGATAGTAAAATCTTTGTTCCAGAGAGAAATAT TTTCTCAATAATTTTCTTACTGCAATGGATTAACGGGTAATATACTAATTGTTCCAATTGTGGATGACAAAATAGGACAACGTTGTTGAGGAAAATTCTGTG atggatcaagitictgaccccicagccagtictalccagcigicaiticiggstcaaacaittgitgaaggaagggccacagittigccittagaaacitt IGGAAGGTACAGGTGAGAT......CTGCAGGTGAGAAGATGGACCAGATGGTCCCTAAGATGCTTCCCAACTTTAGAACTTTAAAAGTTC

gy gy 160 Leu CTG S ty ly Lys Ser Ash Ser Arg Ser Met Agtritication of the Activitication of the Arg Ser Arg Ser Arg Ser Arg

180 Glu Asp Thr Tyr Gly Ile Val Leu Leu Ser Gly Val Lys Tyr Lys Lys Gly Gly Leu Val Ile Asn Glu Thr GAA GAC ACC TAT GGA ATT GTC CYC CYT TCT GGA GTG AAG TAT AAG AAG GGT GGC CTT GTG ATC AAT GAA ACT * Trp

CAC AAG GTC Ser CTC Pro Cys Asn Asn Leu TGC AAC AAC ·CTG Gln Ser CAN TCT 200 ડોડ્રે ઇંડ્રે Leu Tyr Phe Val Tyr Ser Lys Val Tyr Phe Arg CTG TAC TTT GTA TAT TCC AAA GTA TAC TTC CGG 61y 660

Cys Thr. Thr TGC ACT ACT TY. Lys Wet Met Ser Ang ATG ATG AGC 91 90 90 90 Val Met Met Glu GTG ATG ATG GAG Crc Crc Met Arg Asn Ser Lys Tyr Pro Gln Asp ATG AGG AAC TCT AAG TAT CCC CAG GAT . 220 Pyr Tyc

Asp His Leu Tyr Val Asn Val GAT CAT TTA TAT GTC AAC GTA 260 Ala Val Phe Ann Leu Thr Ser Ala GCA GTG TTC AAT CFF ACC AGT GCF * Gln Met Trp Ala Arg Ser Ser Tyr Leu Gly CAG ATG TGG GCC CGC AGC AGC TAC CTG GGG 240

Ser Leu Val Asn Phe Glu Glu Ser Gln Thr Phe Phe Gly Leu Tyr Lys Leu TCT CTG GTC AAT TTF GAG GAA TCT CAG ACG TTF TTC GGC TTA TAT AAG CTC TAA GAGAAGCACTTTGGG 280 Glu Leu GAG CTC Ser

AAGTGGACCTTGAGACCACAGGGTTCAAAATGTCTGTAGCTCCTCAACTCAACTAATGTTTTATGAGCCAGACAAATGGAGGAATATGACGGAAGAACAT ATTICITITICEATTATICATITICTITICAGGCACCGAGAATGTTISTATTICAGTGAGGGTCTTICTTACATGCATTTTGAGGTCAAGTAAGAAGACATGAACC AGAACTCTGGGCTGCCATGTGAAGAGGGAGAAGCATGAAAAAGEAGCTACCAGGTGTTCTACACTCATCTTAGTGCCTGAGAGTATTTAGGCAGATTGA ANAGGACACC

ວຸ	20 Ser Agc	40 Pro	80 Pro	80 G1y GGC	100 G1y GGG	120 Gln CAG	140 Ly 8 AAA	100 Leu CTG
GCTO	Ala GCC	Ar B AGG	Pro	Thr	Leu	Ser Agc	G J u G A A	Pro CCT
Yoo	Ser	Arg Aga	Pro	Ser	61y 660	Thr	Pro	Het ATG
CTCA	Ser	Pro	Pro	His	Leu TTG	Ser TCT	Pro CCC	Ser
CIGA	Asp GAC	Val GTG	Pro	YSU.	GIY	0 1 u	Pro	Ar 8 AGG
5	'A l	Ser. TCT	Pro	01y 666	Yal GTA	Arg CGA	Ser AGT	Ser
GGGT	r Trp V c TGG	The Ser Val	Leu CTA	Arg Gly Aga GGG	Leu TTG	Leu	Pro	Asn Ser Arg Ser Aac TCA Agg TCC
CTGG	77	Pro.	Pro	Lys AAG	Ala	61u 61u	His	Ser TCC
TT G	11e ATC	Cys TGT	Pro	Lys AAG	γα] GTT	A.1 a GCA	6.1 y	Lys AAG
CCGT	Gln CAG	Pro	Pro	Leu CTG	Leu CTG	Leu CTG	11e ATA	61y 660
CTACAGGACT GAGAAGAAGT AAAACCGTTT GCTGGGGGTG GCCTGACTCA CCAGGTGCC	10 Pro	30 Leu CTT	60 Pro CCA	70 Pro	90 Yal GTT	110 Glu GAG	130 Gln CAA	150 Thr ACA
AGT	Tyr TAT	Val GTT	Pro	Pro	Het ATG	Lys λλG	Lys AAG	Leu TTA
YYYGY	Pro	Thr	Pro Pro Pro CCA CCA CCA	Leu CTG	Phe TTC	Gln	61u GAG	His
DY9 .	Tyr Tag	61y 660	Pro CCA·	Pro	Phe TTT	Leu CTÅ	Leu TTG	Ala GCC
GACT	Asn AAT	Pro	Pro CCA	Leu	Het Phe ATG TTT	His	Ser Leu TCT TTG	Lys Yal Ala His AAA GTG GCC CAT
YOY!	Phe TTC	Pro	Pro	Pro CCA	Val GTG	Phe TTC	Ser TCA	Lys AAA
2	Pro CCC	Ala GCC	Arg AGG	Pro CCT	Leu	Leu CTC	λ1α GCA	λιε λ66
	Gln CAG	Trp TGG	Arg	Leu CTG	Leu	Gln	Thr Aca	Leu CTG
	Gln CAG	P 1.0	Gln CAA	Pro	Cys TGT	Phe TIT	His	Glu Leu GAG CTG
	Het ATG	Ser	61y 66T	Pro	Leu CTG	Жet ЛТG	Жet ЛТG	Lys λλG

EP 0 675 200 A1

FIG. 2(

180 Gly GGC	200 Gln CAA	220 Gln CAG	240 A1a GCC	200 Asn AAC	280 Lys AAG
617	Gly	Pro 000		Val GTC	Tyr Tat
Lys	Ark	Tyr	Χet λTG	Tyr Tat	Leu TTA
Lys AAG	Phe TTC	Eys AAG	Gln CAG	Leu TTA	613
Tyr Tat	Tyr Tac	Ser	613	His Cat	Phe TTC
Lys Aag	Val GTÅ	Ash		As p GAT	
γαl GTG	Lys AAA	Ar 8 AGG		Ala GCT	Thr
61 <i>y</i> .66Å	Ser ICC		Cys TGC	Ser AGT	Gln CAG
Ser TCT	Tyr TAT	Tyr Tac	ΤΥΓ ΤΑC	Thr	Ser TCT
Leu CTT	γα1 GTA	Val GTC	Ser	Leu	61u GAA
170 Leu CTG	190 Phe IIT	210 Lys λλG	230 Het ATG	260 Asn AAT	270 Glu GAG
Val GTC	Tyr Tac	His			Phe TTT
I 1 e A T T	Leu CTG	Ser AGC	Ly.s AAG		Asn
G 1 y G G A	61y 666		617	λ1α GCA	Val GTC
Tyr Tat	Thr	014	6 1 u G A G	6 1 y 6 6 C	Leu
Thr	61u 6AA	Leu CTG	Het ATG	Leu CTG	Ser TCT
Asp GAC	Asn	YYC	Het ATG	Tyr Tac	Leu CTC
G 1 u G A A	11e ATC	ASn	Val GTG	Ser	61u 646
Trp	γa] GTG	Cys TGC	Leu CTG	Ser	Ser TCT
61u 6AA	Leu	Ser	Asp GAT	Arg	γal GTA

Leu CTC TAA GAGAAGCACTTTGGGATTÇ

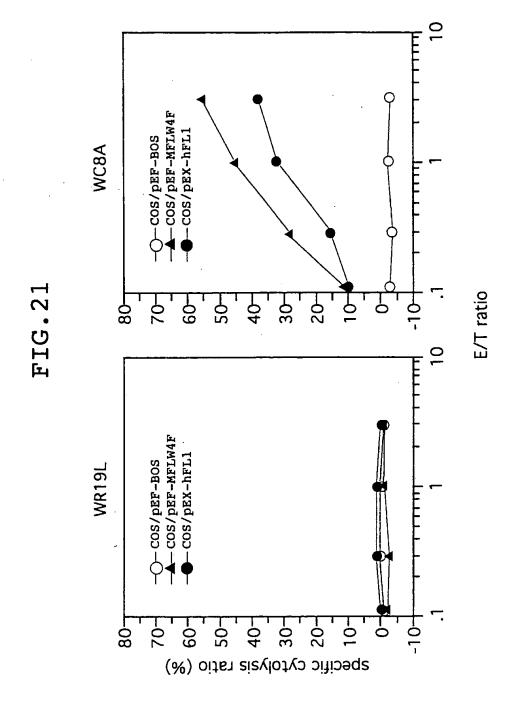
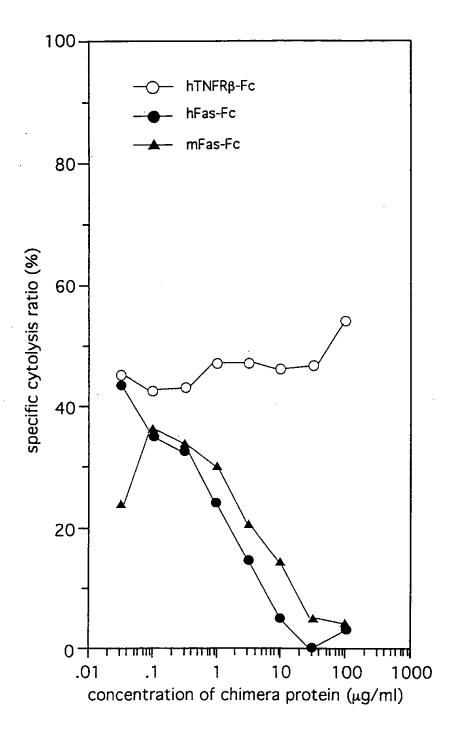


FIG.22



CIGCGGAAACTITATAAAGAAAACT

TAGCTTCTCTGGAGCAGTCAGCGTCTGTCTTGACACTGAGTCTCCTCCACAAGGCTGTGAGAAAGGAAACCCTTTCCTGGGGCTGGGTGCC	AGT GCC ACT TCA TCT TGG GCT CCT Ser Ala Thr Ser Ser Trp Ala Pro	CAA AGG AGA CCG CCA CCT CCA CCA CCA Gln Arg Arg Pro Pro Pro Pro	ACC CCT CTA AAG AAG AAG GAC CAC Thr Pro Leu Lys Lys Lys Asp His	TTT TTC ATG GTT CTG GTT GCT CTG GTT GGA ATG GGA TTA GGA ATG TAT. Phe Phe Met Val Lew Val Ala Lew Val Gly Met Gly Lew Gly Met Tyr	CTC CGT GAG TTC ACC AAC CAA AGC CTT AAA GTA TCA TCT TTT Leu Arg Glu Phe Thr Asn Gln Ser Leu Lys Val Ser Ser Phe	CCG AGG AGT GTG GCC CAT TTA ACA GGG AAC Pro Arg Ser Val Ala His Leu Thr Gly Asn	CTG ATC TCT GGA GTG AAG TAT AAG Leu Ile Ser Gly Val Lys Tyr Lys	TCC AAA GTA TAC TTC CGG GGT CAG TCT TGC Ser Lys Val Tyr Phe Arg Gly Gln Ser Cys
ACA	GTA GAC AGC Val. Asp Ser	CCG GAC (Pro Asp (CCG CCA CTG Pro Pro Leu	27	IC Je	GAG CCG Glu Pro	GGA ACC Gly Thr	TAT 1 Tyr s
TCC	2 S	2 2 2 2		9 H	14 A 29 P	0 5 5	. F. F.	ਦ <i>ਦ</i> 2ਰ
CTCC	TGG Trp	00 1	CCA. CTG Pro Leu	23	r G)	₹ ₹	£ £	TTC GTG Phe Val
AGT(TTC	AG) Arç		Z G	Arg	gaa aaa aaa Glu Lys Lys	Thursday.	P. P. P.
CTG	ATC Ile	CCT	CTC	ATG	CTC Leu	GAA Glu	GAC Asp	TAC
BACA	CAG ATC Gln Ile	GGG CCT AGA GGG Gly Pro Arg Gly	CCA Pro	TTC	GAA	TCT Ser	GAA GAC ACA TAT Glu Asp Thr Tyr	TTG TAC
CTT	CCC	TGT Cys	CAA Gin	TTT	GCA	CCC	TGG Trp	666
TOT	TGT Cys	CCA 1CT Pro Ser	TCA	GTA Val		CCC AGT ACA Pro Ser Thr	GAA	AAC GAA ACT GGG Asn Glu Thr Gly
GTTC	CCA Pro	CCA Pro	CCA	STC Val	AAG GAA CTG Lys Glu Leu	AGT Ser	CTG	GAA Glu
C)C)	TAC Tyr	TGT Cys	CCG Pro	ccc crc Pro Val	AAG Lys	CCC	CCT Pro	AAC Asn
GCGT	AAT Asn	CCC	CCA	CTA Len	CAG Gln	GCC. AAC Ala Asn	ATC Ile	ATC
3TCA	ATG	TTT	CTA	TGG	CTG Leu	SCC.	TCC.	GTG
VGCA(TC 7		TA (CTT (Leu 1
TGG	CAG (TCA GTT Ser Val	TCA CCA Ser Pro	AT C	TTC CAC Phe His	CAA ATA Gln Ile	TCA AGG Ser Arg) 256 1 \(\frac{1}{1} \)
MCT	CAG CAG CCC Gln Gln Pro	666 1 61y s	GTG T Val S	ACA AAT CTG Thr Asn <u>Ley</u>	CTC 1 Leu P	AAG C Lys G	CAC 1 His S	GGT GGC Gly 1
AGCJ	ATG C Wet G	CCA G Pro G	CCT G Pro V	AAC A Asn T	CAG C	GAA A Glu L	CCC C Pro H	AAA G Lys G
H	< I	U p.	OA	< <	U	g g	Ua,	∢ ∑

GAG Glu GNG Glu ATG Wet CTA Sa) Va) TAT ATG AGG AAC TCT AAG TAT CCT GAG GAT CTG TYR Met Arg Asn Ser Lys Tyr Pro Glu Asp Leu AAC AAC CAG CCC CTA AAC CAC AAG GTC Asn Asn Gln Pro Leu Asn His Lys Val

A TTC AAT CTT ACC. The Asn Leu Thr AGG TTG AAC TAC TGC ACT ACT GGA CAG ATA TGG GCC CAC AGC AGC TAC CTG GGG GCA GTA Arg Leu Asn Tyr Cys Thr Thr Gly Gln Ile Trp Ala His Ser Ser Tyr Leu Gly Ala Val NAG Lys

CAT TTA TAT GTC AAC ATA TCT CAA CTC TCT CTG ATC AAT 11T GAG GAA TCT AAG ACC TTT TTC GGC GAC Asp GCT Ala AGT Ser

TIG TAT ANG CIT TAA AAGAAAAGCATITTAAAATGATCTACTATTCTITAATGGGCACCAGGAATAITGTCTTGAATGAGAGTCTTCTTAA Leu Tyr Lys Leu

GACCTATIGAGATTAATTAAGACTACATGAGCCACAAAGACCTCATGACCGCAAGGTCCAACAGGTCAGCTATCCTTCATTTTCTCGAGGTCCATGGAG TGGTCCTTAATGCCTGCATCATGAGGCAGATGGAAGGAGGTCTGTGACTGAGGGACATAAAGCTTYGGGCTGCTGTGTGTGACAATGCAGAGGCACAGAGA AAGAACTGTCTGATGTTAAATGGCCAAGAGAATTTTAACCATTGAAG----AAGACACCTTTACACTCA-CTTCCAGGGTGGGTCTACTTACTACCTCA GTGTCTCATTGGCACCATCTTTACTGTTACCTAAATGTTTTCTGAGCCGACCTTTGATCCTAACGGAGAAGTAAAGAGGGATGTTTGAGGCACAAAATCATT CICTACATAGCATGCATACCTCCAGTGCAATGATGTCTGTGTGT---TTGTATGTATGAAGCAAACAGATTCTAAAGAGTCATATA<u>AATAAAA</u>TATGTA CATTATGGAGTACATATTAGAAACC----TGTTACATTTGGTGCTAGA-TATCTGGAATGTTTTGGC<u>AATAAA</u>CTCTAATAGTCT

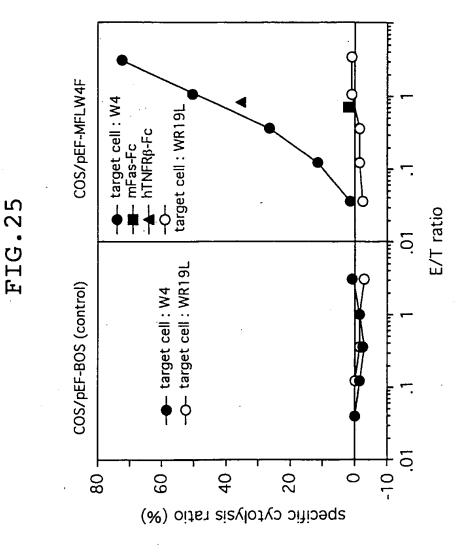


FIG.26

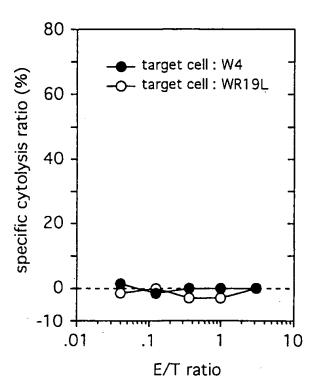
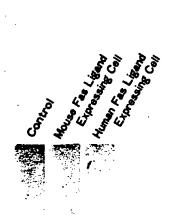
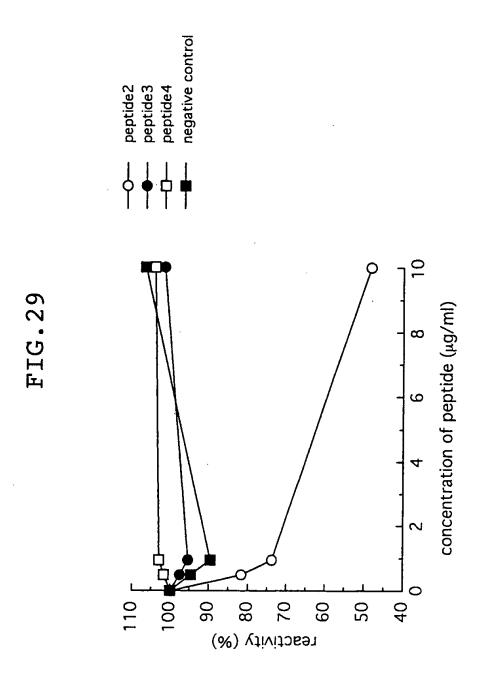


FIG.27







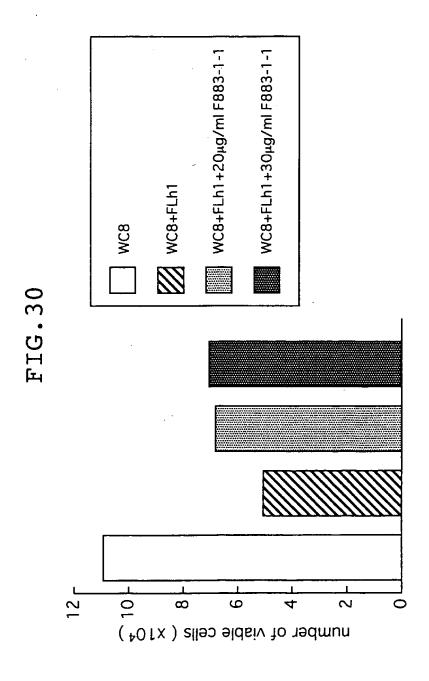


FIG.31

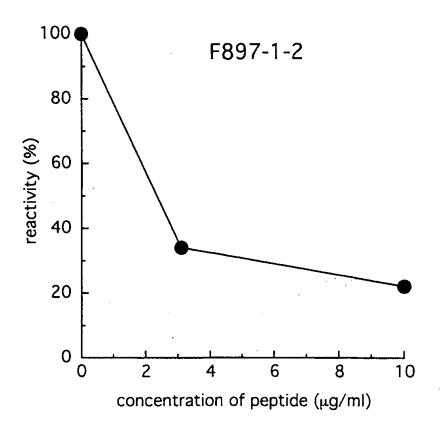
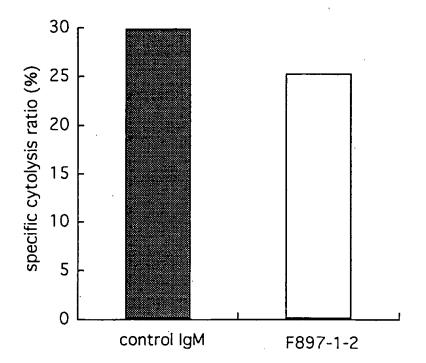
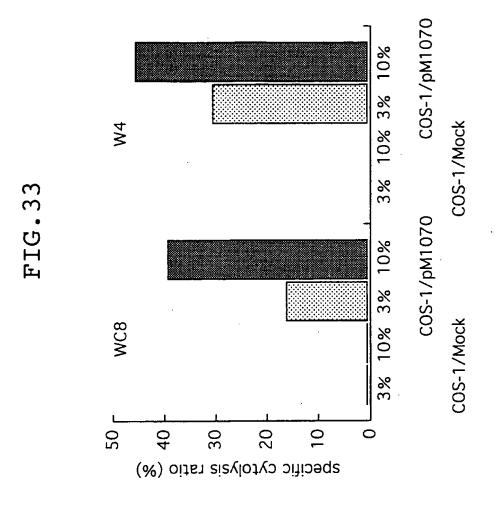


FIG.32





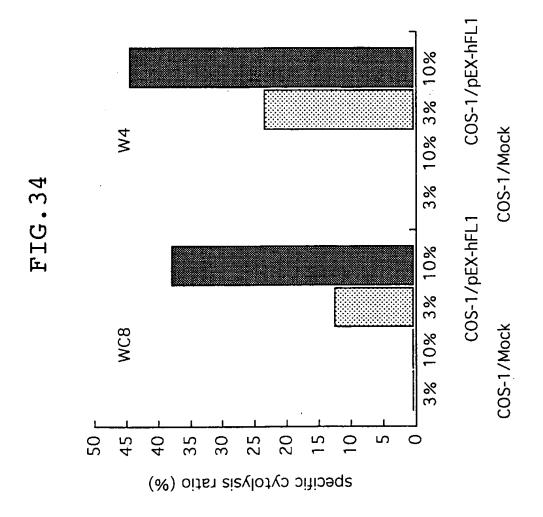
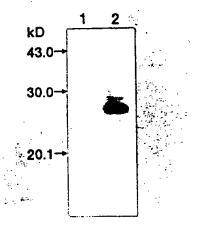


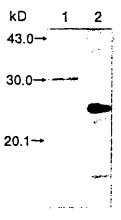
FIG.35



1: Mock

2:COS-1/pM1070

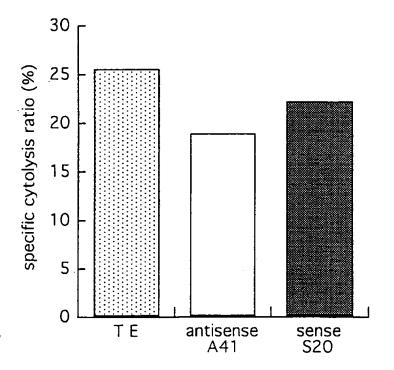
FIG.36

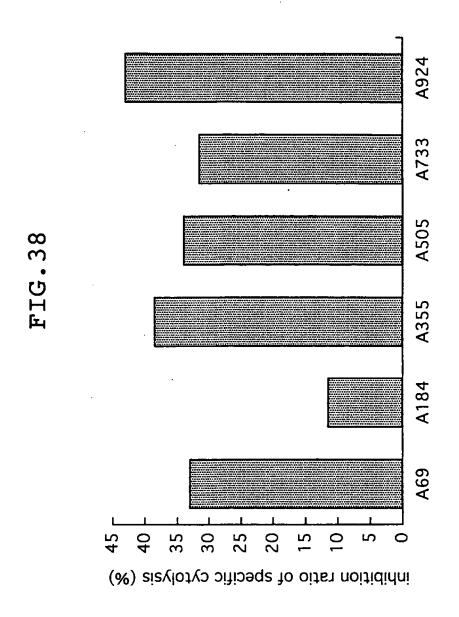


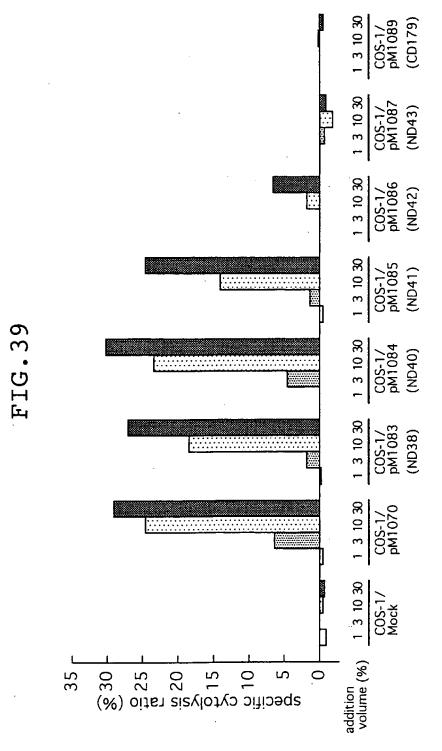
1: Mock

2:COS-1/pEX-hFL1

FIG.37

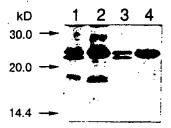






concentration of culture sup of recombinant cells

FIG.40



1: JE5505(pM1068) Cell DTT(+)
2: JE5505(pM1068) Cell DTT(+)
3: JE5505(pM1068) Sup DTT(-)
4: JE5505(pM1068) Sup DTT(+)



- 1: JE5505(pM1069) Cell DTT(-) 2: JE5505(pM1069) Cell DTT(+)
- 3: JE5505(pM1069) Sup DTT(-)
- 4: JE5505(pM1069) Sup DTT(十)

EUROPEAN SEARCH REPORT

EP 94 11 7761

	DOCUMENTS CONS			
Category	Citation of document with of relevant p	indication, where appropriate,	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.CL6)
P,X	US pages 1169 - 1178 SUDA T. ET AL. 'Mo expression of the f member of the tumor family' * the whole document J. EXP. MED.,	r necrosis factor	1-57	C12N15/19 C07K14/52 C12N15/62 C12N1/21 C12N1/19 C12N5/10 C07K16/24 C12N15/11 G01N33/68
	vol.179, March 1994 pages 873 - 879 SUDA T. ET AL. 'Pur characterization of induces apoptosis' * the whole document	rification and f the Fas-ligand that		·
P,X	CELL, vol.76, 25 March 19 pages 969 - 976 TAKAHASHI T. ET AL. lymphoproliferative caused by a point m ligand' * the whole documen	e disease in mice, mutation in the Fas	1-57	TECHNICAL FIELDS SEARCHED (Int.Cl.4) C12N C07K G01N
P,X	NATURE, vol.367, 27 January pages 317 - 318 CORY S. 'Fascinatin' * the whole documer	ng death factor'	1-57	
	The present search report has i	been drawn up for all claims Date of completion of the search		Econolium
	THE HAGUE	1 August 1995	Esp	en, J
X : part Y : part doc: A : tech O : non	CATEGORY OF CITED DOCUME icularly relevant if taken alone toularly relevant if combined with an ament of the same category an along a background written discourse mediate document	NTS T: theory or princi E: earlier patent di after the filing d	ple underlying the comment, but published in the application for other reasons	invention isbel on, or

EPO PORM 1500 00.42 (POICOL)

Category	Citation of document with indica of relevant passage	tion, where appropriate,	Relevant to claim	CLASSIFICATION OF THE APPLICATION (Int.Cl.6)
D,A	CELL, vol.66, 1991, CAMBRIDG pages 233 - 243 ITOH N. ET AL. 'The po the cDNA fro human cel Fas can mediate apopto * the whole document *	E, NA US Typeptide encoded by Surface antigen sis'		
A	WO-A-91 10488 (GERMAN CENTER) 25 July 1991 * the whole document *			
A	EP-A-0 510 691 (OSAKA INSTITUTE) 28 October * the whole document *	1992		
				TECHNICAL FIELDS SEARCHED (Int.CL6)
			-	
	The present search report has been o	rawn up for all claims		
	Place of search	Date of completion of the search	<u> </u>	Rimin
	THE HAGUE	1 August 1995	Esp	en, J
X : part Y : part doc	CATEGORY OF CITED DOCUMENTS ticularly relevant if taken alone ticularly relevant if combined with another unsent of the same category anological background	T: theory or principle E: earlier parent door sfre the filing du D: focument cited in L: document cited fo	underlying the ment, but public te the application	investice ished on, or